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(54) Title: POLYNUCLEOTIDES ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE (57) Abstract Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.		

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POLYNUCLEOTIDES ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE

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Technical Field of the Invention

This invention relates to polynucleotides encoding polypeptides, polypeptides expressed in skin cells, and their use in therapeutic methods.

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Background of the Invention

The skin is the largest organ in the body and serves as a protective cover. The loss of skin, as occurs in a badly burned person, may lead to death owing to the absence of a barrier against infection by external microbial organisms, as well as loss of body temperature and body fluids.

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Skin tissue is composed of several layers. The outermost layer is the epidermis which is supported by a basement membrane and overlies the dermis. Beneath the dermis is loose connective tissue and fascia which cover muscles or bony tissue. The skin is a self-renewing tissue in that cells are constantly being formed and shed. The deepest cells of the epidermis are the basal cells, which are enriched in cells capable of replication. Such replicating cells are called progenitor or stem cells. Replicating cells in turn give rise to daughter cells called 'transit amplifying cells'. These cells undergo differentiation and maturation into keratinocytes (mature skin cells) as they move from the basal layer to the more superficial layers of the epidermis. In the process, keratinocytes become cornified and are ultimately shed from the skin surface. Other cells in the epidermis include melanocytes which synthesize melanin, the pigment responsible for protection against sunlight. The Langerhans cell also resides in the epidermis and functions as a cell which processes foreign proteins for presentation to the immune system.

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The dermis contains nerves, blood and lymphatic vessels, fibrous and fatty tissue. Within the dermis are fibroblasts, macrophages and mast cells. Both the epidermis and dermis are penetrated by sweat, or sebaceous, glands and hair follicles. Each strand of

hair is derived from a hair follicle. When hair is plucked out, the hair re-grows from epithelial cells directed by the dermal papillae of the hair follicle.

When the skin surface is breached, for example in a wound, the stem cells proliferate and daughter keratinocytes migrate across the wound to reseal the tissues. The skin cells therefore possess genes activated in response to trauma. The products of these genes include several growth factors, such as epidermal growth factor, which mediate the proliferation of skin cells. The genes that are activated in the skin, and the protein products of such genes, may be developed as agents for the treatment of skin wounds. Additional growth factors derived from skin cells may also influence growth of other cell types. As skin cancers are a disorder of the growth of skin cells, proteins derived from skin that regulate cellular growth may be developed as agents for the treatment of skin cancers. Skin derived proteins that regulate the production of melanin may be useful as agents which protect skin against unwanted effects of sunlight.

Keratinocytes are known to secrete cytokines and express various cell surface proteins. Cytokines and cell surface molecules are proteins which play an important role in the inflammatory response against infection and also in autoimmune diseases affecting the skin. Genes and their protein products that are expressed by skin cells may thus be developed into agents for the treatment of inflammatory disorders affecting the skin.

Hair is an important part of a person's individuality. Disorders of the skin may lead to hair loss. Alopecia areata is a disease characterized by the patchy loss of hair over the scalp. Total baldness is a side effect of drug treatment for cancer. The growth and development of hair are mediated by the effects of genes expressed in skin and dermal papillae. Such genes and their protein products may be usefully developed into agents for the treatment of disorders of the hair follicle.

New treatments are required to hasten the healing of skin wounds, to prevent the loss of hair, enhance the re-growth of hair or removal of hair, and to treat autoimmune and inflammatory skin diseases more effectively and without adverse effects. More effective treatments of skin cancers are also required. There thus remains a need in the art for the identification and isolation of genes encoding proteins expressed in the skin, for use in the development of therapeutic agents for the treatment of disorders including those associated with skin.

Summary of the Invention

The present invention provides polypeptides expressed in skin cells, together with polynucleotides encoding such polypeptides, expression vectors and host cells comprising such polynucleotides, and methods for their use.

In specific embodiments, isolated polynucleotides are provided that comprise a DNA sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (b) complements of the sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (c) reverse complements of the sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (d) reverse sequences of the sequences recited in SEQ ID NO: 1-14, 45-48, 64-68, 77-89, 118, 119, 198-231, 239-249, 254-274, 349-372 and 399-405; (e) sequences having a 99% probability of being the same as a sequence of (a)-(d); and (f) sequences having at least 50%, 75% or 90% identity to a sequence of (a)-(d).

In further embodiments, the present invention provides isolated polypeptides comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409, together with isolated polynucleotides encoding such polypeptides. Isolated polypeptides which comprise at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409; and (b) sequences having 50%, 75% or 90% identity to a sequence of SEQ ID NO: 120-197, 275-348, 373-398 and 406-409 are also provided.

In related embodiments, the present invention provides expression vectors comprising the above polynucleotides, together with host cells transformed with such vectors.

In a further aspect, the present invention provides a method of stimulating keratinocyte growth and motility, inhibiting the growth of epithelial-derived cancer cells,

inhibiting angiogenesis and vascularization of tumors, or modulating the growth of blood vessels in a subject, comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 187, 196, 342, 343, 395, 397, and 398; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 187, 196, 342, 343, 395, 397, and 398.

Methods for modulating skin inflammation in a subject are also provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 338 and 347; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 338 and 347. In an additional aspect, the present invention provides methods for stimulating the growth of epithelial cells in a subject. Such methods comprise administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 129 and 348; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 129 and 348. In yet a further aspect, methods for inhibiting the binding of HIV-1 to leukocytes, for the treatment of an inflammatory disease or for the treatment of cancer in a subject are provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 340, 344, 345 and 346; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NO: 340, 344, 345 and 346.

As detailed below, the isolated polynucleotides and polypeptides of the present invention may be usefully employed in the preparation of therapeutic agents for the treatment of skin disorders.

The above-mentioned and additional features of the present invention, together with the manner of obtaining them, will be best understood by reference to the following more detailed description. All references disclosed herein are hereby incorporated herein by reference in their entirety as if each was incorporated individually.

Brief Description of the Drawings

Fig. 1 shows the results of a Northern analysis of the distribution of huTR1 mRNA in human tissues. Key: He, Heart; Br, Brain; Pl, Placenta; Lu, Lung; Li, Liver;
5 SM, Skeletal muscle; Ki, Kidney; Sp, Spleen; Th, Thymus; Pr, Prostate; Ov, Ovary.

Fig. 2 shows the results of a MAP kinase assay of muTR1a and huTR1a. MuTR1a (500ng/ml), huTR1a (100ng/ml) or LPS (3pg/ml) were added as described in the text.

Fig. 3 shows the stimulation of growth of neonatal foreskin keratinocytes by
10 muTR1a.

Fig. 4 shows the stimulation of growth of the transformed human keratinocyte cell line HaCaT by muTR1a and huTR1a.

Fig. 5 shows the inhibition of growth of the human epidermal carcinoma cell line A431 by muTR1a and huTR1a.

15 Fig. 6 shows the inhibition of IL-2 induced growth of concanavalin A-stimulated murine splenocytes by KS2a.

Fig. 7 shows the stimulation of growth of rat intestinal epithelial cells (IEC-18) by a combination of KS3a plus apo-transferrin.

Fig. 8 illustrates the oxidative burst effect of TR-1 (100 ng/ml), muKS1
20 (100 ng/ml), SDF1 α (100 ng/ml), and fMLP (10 μ M) on human PBMC.

Figure 9 shows the chemotactic effect of muKS1 and SDF-1 α on THP-1 cells.

Figure 10 shows the induction of cellular infiltrate in C3H/HeJ mice after intraperitoneal injections with muKS1 (50 μ g), GV14B (50 μ g) and PBS.

Figure 11 demonstrates the induction of phosphorylation of ERK1 and ERK2 in
25 CV1/EBNA and HeLa cell lines by huTR1a.

Figure 12 shows the huTR1 mRNA expression in HeLa cells after stimulation by muTR1, huTR1, huTGF α and PBS (100 ng/ml each).

Figure 13 shows activation of the SRE by muTR1a in PC-12 (Fig. 13a) and HaCaT (Fig. 13b) cells.

Figure 14 shows the inhibition of huTR1a mediated growth on HaCaT cells by an antibody to the EGF receptor.

Detailed Description of the Invention

In one aspect, the present invention provides polynucleotides that were isolated
5 from mammalian skin cells. As used herein, the term "polynucleotide" means a single or
double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes
DNA and RNA molecules, both sense and anti-sense strands. The term comprehends
cDNA, genomic DNA, recombinant DNA and wholly or partially synthesized nucleic
acid molecules. A polynucleotide may consist of an entire gene, or a portion thereof. A
10 gene is a DNA sequence that codes for a functional protein or RNA molecule. Operable
anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide,
and the definition of "polynucleotide" therefore includes all operable anti-sense
fragments. Anti-sense polynucleotides and techniques involving anti-sense
polynucleotides are well known in the art and are described, for example, in Robinson-
15 Benion et al., "Anti-sense Techniques," *Methods in Enzymol.* 254(23):363-375, 1995;
and Kawasaki et al., *Artific. Organs* 20 (8):836-848, 1996.

Identification of genomic DNA and heterologous species DNAs can be
accomplished by standard DNA/DNA hybridization techniques, under appropriately
stringent conditions, using all or part of a cDNA sequence as a probe to screen an
20 appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are
designed based on known genomic DNA, cDNA and protein sequences can be used to
amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to
the identified sequences and variants may be produced by conventional synthesis
methods. All the polynucleotides provided by the present invention are isolated and
25 purified, as those terms are commonly used in the art.

In specific embodiments, the polynucleotides of the present invention comprise a
DNA sequence selected from the group consisting of sequences provided in SEQ ID NO:
1-119, 198-274, 349-372 and 399-405, and variants of the sequences of SEQ ID NO:
1-119, 198-274, 349-372 and 399-405. Polynucleotides that comprise complements of
30 such DNA sequences, reverse complements of such DNA sequences, or reverse

sequences of such DNA sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement," "reverse complement," and "reverse sequence," as used herein, is best illustrated by the following example. For the sequence
 5 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

10 In another aspect, the present invention provides isolated polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides
 15 encoded by a polynucleotide which comprises a partial isolated DNA sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409, as well as variants of such sequences.

Polypeptides of the present invention may be produced recombinantly by
 20 inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide.
 25 Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional
 30 portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 120-197, 275-348, 373-398, 406-409,

and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or
5 more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide
10 fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using
15 techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is
20 commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, T., *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequence
25 may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure. In
30 certain preferred embodiments, described in detail below, the isolated polypeptides are

incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide or polypeptide sequences may be aligned, and percentage of identical nucleotides in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The alignment and similarity of polypeptide sequences may be examined using the BLASTP and algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>) under /blast/executables/. The FASTA and FASTX algorithms are available on the Internet at the ftp site <ftp://ftp.virginia.edu/pub/>. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX v1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is also described in Pearson, WR and Lipman, DJ, "Improved Tools for Biological Sequence Analysis," *PNAS* 85:2444-2448, 1988; and Pearson WR, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," *Methods in Enzymology* 183:63-98, 1990.

The BLASTN algorithm version 2.0.4 [Feb-24-1998], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm version 2.0.4, set to the default parameters described
 5 in the documentation and distributed with the algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX is described at NCBI's website at URL <http://www.ncbi.nlm.nih.gov/BLAST/newblast.html> and in the publication of Altschul, Stephen F., *et al.*, "Gapped BLAST and PSI-BLAST: a new
 10 generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with default parameters thus: `blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results`; and parameters are: -p
 15 Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out]
 20 Optional. The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity for polypeptides: `blastall -p blastp -d swissprot -e 10 -G 1 -E 11 -r 1 -v 30 -b 30 -i queryseq -o results`; and the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes
 25 default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out]
 Optional.

The "hits" to one or more database sequences by a queried sequence produced by
 30 BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of

sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The percentage similarity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage similarity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The similarity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing
5 an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred
10 embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a
15 sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

Variant polynucleotide sequences will generally hybridize to the recited
20 polynucleotide sequences under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

25 As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide or polypeptide, respectively, comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372 and 399-405; or any of the polypeptides set out in SEQ ID NO: 120-197, 275-348, 373-398 and 406-409. The value of x may be from about 20 to about
30 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (x -mers) of any of the polynucleotides identified as SEQ ID NO: 1-119, 198-274, 349-372 and 399-405, or their variants. Polypeptides of the present invention comprehend polypeptides comprising at least a
5 specified number of contiguous residues (x -mers) of any of the polypeptides identified as SEQ ID NO: 120-197, 275-348, 373-398, and 406-409. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a
10 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NO: 1-119, 198-274, 349-372 and 399-405 or a variant of one of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a
15 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, or a variant of one of the polynucleotides provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409.

The inventive polynucleotides may be isolated by high throughput sequencing of
20 cDNA libraries prepared from mammalian skin cells as described below in Example 1. Alternatively, oligonucleotide probes based on the sequences provided in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405 can be synthesized and used to identify positive clones in either cDNA or genomic DNA libraries from mammalian skin cells by means of hybridization or polymerase chain reaction (PCR) techniques. Probes can be shorter than
25 the sequences provided herein but should be at least about 10, preferably at least about 15 and most preferably at least about 20 nucleotides in length. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR Technology*, Stockton Press: NY, 1989; (Sambrook, J, Fritsch, EF and
30 Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring

Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

In addition, DNA sequences of the present invention may be generated by synthetic means using techniques well known in the art. Equipment for automated
5 synthesis of oligonucleotides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems Division (Foster City, California) and may be operated according to the manufacturer's instructions.

Since the polynucleotide sequences of the present invention have been derived from skin, they likely encode proteins that have important roles in growth and
10 development of skin, and in responses of skin to tissue injury and inflammation as well as disease states. Some of the polynucleotides contain sequences that code for signal sequences, or transmembrane domains, which identify the protein products as secreted molecules or receptors. Such protein products are likely to be growth factors, cytokines, or their cognate receptors. Several of the polypeptide sequences have more than 25%
15 similarity to known biologically important proteins and thus are likely to represent proteins having similar biological functions.

In particular, the inventive polypeptides have important roles in processes such as: induction of hair growth; differentiation of skin stem cells into specialized cell types; cell migration; cell proliferation and cell-cell interaction. The polypeptides are important in
20 the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of the disclosed polypeptides act as modulators of immune responses, especially since immune cells are known to infiltrate skin during tissue insult causing growth and differentiation of skin cells. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of
25 disease states not only within skin, but also in other tissues of the body. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

In one aspect, the present invention provides methods for using one or more of the
30 inventive polypeptides or polynucleotides to treat disorders in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human.

In this aspect, the polypeptide or polynucleotide is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may
5 comprise one or more of the above polypeptides and a non-specific immune response amplifier, such as an adjuvant or a liposome, into which the polypeptide is incorporated.

Alternatively, a vaccine or pharmaceutical composition of the present invention may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines and pharmaceutical compositions, the
10 DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, and bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as
15 *Bacillus-Calmette-Guerin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other poxvirus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA into such expression systems are well known in the
20 art. The DNA may also be "naked," as described, for example, in Ulmer, *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from
25 individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous, or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg per
30 kg of host, and preferably from about 100 pg to about 1 µg per kg of host. Suitable dose

sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax, or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of adjuvants may be employed in the vaccines derived from this invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *M. tuberculosis*. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories, Detroit, Michigan), and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, New Jersey). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, and Quil A.

The polynucleotides of the present invention may also be used as markers for tissue, as chromosome markers or tags, in the identification of genetic disorders, and for the design of oligonucleotides for examination of expression patterns using techniques well known in the art, such as the microarray technology available from Synteni (Palo Alto, California). Partial polynucleotide sequences disclosed herein may be employed to obtain full length genes by, for example, screening of DNA expression libraries using hybridization probes or PCR primers based on the inventive sequences.

The polypeptides provided by the present invention may additionally be used in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, in assays to quantitatively determine levels of protein or cognate

corresponding ligand or receptor, as anti-inflammatory agents, and in compositions for skin, connective tissue and/or nerve tissue growth or regeneration.

Example 1

5 ISOLATION OF cDNA SEQUENCES FROM SKIN CELL EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed from specialized rodent or human skin cells as shown in Table 1.

10

Table 1

Library	Skin cell type	Source
DEPA	dermal papilla	rat
SKTC	keratinocytes	human
HNFF	neonatal foreskin fibroblast	human
15 MEMS	embryonic skin	mouse
KSCL	keratinocyte stem cell	mouse
<u>TRAM</u>	<u>transit amplifying cells</u>	<u>mouse</u>

These cDNA libraries were prepared as described below.

20 cDNA Library from Dermal Papilla (DEPA)

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA Library from Keratinocytes (SKTC)

Keratinocytes obtained from human neonatal foreskins (Mitra, R and Nikoloff, B in *Handbook of Keratinocyte Methods*, pp. 17-24, 1994) were grown in serum-free KSFM (BRL Life Technologies) and harvested along with differentiated cells (10^8 cells). Keratinocytes were allowed to differentiate by addition of fetal calf serum at a final

concentration of 10% to the culture medium and cells were harvested after 48 hours. Total RNA was isolated from the two cell populations using TRIzol Reagent (BRL Life Technologies) and used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene). cDNAs expressed in differentiated keratinocytes were enriched by using a
5 PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, California). Briefly, mRNA was obtained from either undifferentiated keratinocytes ("driver mRNA") or differentiated keratinocytes ("tester mRNA") and used to synthesize cDNA. The two populations of cDNA were separately digested with *RsaI* to obtain shorter, blunt-ended molecules. Two tester populations were created by ligating different adaptors at the
10 cDNA ends and two successive rounds of hybridization were performed with an excess of driver cDNA. The adaptors allowed for PCR amplification of only the differentially expressed sequences which were then ligated into T-tailed pBluescript (Hadjeb, N and Berkowitz, GA, *BioTechniques* 20:20-22 1996), allowing for a blue/white selection of cells containing vector with inserts. White cells were isolated and used to obtain plasmid
15 DNA for sequencing.

cDNA library from human neonatal fibroblasts (HNFF)

Human neonatal fibroblast cells were grown in culture from explants of human neonatal foreskin and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies,
20 Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA library from mouse embryonic skin (MEMS)

25 Embryonic skin was micro-dissected from day 13 post coitum Balb/c mice. Embryonic skin was washed in phosphate buffered saline and mRNA directly isolated from the tissue using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

30 cDNA library from mouse stem cells (KSCL) and transit amplifying (TRAM) cells

Pelts obtained from 1-2 day post-partum neonatal Balb/c mice were washed and

incubated in trypsin (BRL Life Technologies) to separate the epidermis from the dermis. Epidermal tissue was disrupted to disperse cells, which were then resuspended in growth medium and centrifuged over Percoll density gradients prepared according to the manufacturer's protocol (Pharmacia, Sweden). Pelleted cells were labeled using
5 Rhodamine 123 (Bertoncello I, Hodgson GS and Bradley TR, *Exp Hematol.* 13:999-1006, 1985), and analyzed by flow cytometry (Epics Elite Coulter Cytometry, Hialeah, Florida). Single cell suspensions of rhodamine-labeled murine keratinocytes were then labeled with a cross reactive anti-rat CD29 biotin monoclonal antibody (Pharmingen, San Diego, California; clone Ha2/5). Cells were washed and incubated with anti-mouse
10 CD45 phycoerythrin conjugated monoclonal antibody (Pharmingen; clone 30F11.1, 10ug/ml) followed by labeling with streptavidin spectral red (Southern Biotechnology, Birmingham, Alabama). Sort gates were defined using listmode data to identify four populations: CD29 bright rhodamine dull CD45 negative cells; CD29 bright rhodamine bright CD45 negative cells; CD29 dull rhodamine bright CD45 negative cells; and CD29
15 dull rhodamine dull CD45 negative cells. Cells were sorted, pelleted and snap frozen prior to storage at -80°C. This protocol was followed multiple times to obtain sufficient cell numbers of each population to prepare cDNA libraries. Skin stem cells and transit amplifying cells are known to express CD29, the integrin $\beta 1$ chain. CD45, a leucocyte
20 specific antigen, was used as a marker for cells to be excluded in the isolation of skin stem cells and transit amplifying cells. Keratinocyte stem cells expel the rhodamine dye more efficiently than transit amplifying cells. The CD29 bright, rhodamine dull, CD45 negative population (putative keratinocyte stem cells; referred to as KSCL), and the CD29 bright, rhodamine bright, CD45 negative population (keratinocyte transit amplifying cells; referred to as TRAM) were sorted and mRNA was directly isolated
25 from each cell population using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Perkin Elmer/Applied Biosystems Division Prism 377
30 sequencer.

Example 2CHARACTERIZATION OF ISOLATED CDNA SEQUENCES

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithms FASTA and/or BLASTN. The corresponding
5 predicted protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the computer algorithms FASTX and/or BLASTP. Comparisons of DNA sequences provided in SEQ ID NO: 1-119 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 120-197 to sequences in the SwissProt database (using FASTX)
10 were made as of March 21, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 198-274 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 275-348 to sequences in the SwissProt database (using BLASTP) were made as of October 7, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 349-372 to sequences in the EMBL DNA database (using
15 BLASTN) and amino acid sequences provided in SEQ ID NO: 373-398 to sequences in the SwissProt database (using BLASTP) were made as of January 23, 1999.

Isolated cDNA sequences and their corresponding predicted protein sequences were computer analyzed for the presence of signal sequences identifying secreted molecules. Isolated cDNA sequences that have a signal sequence at a putative start site
20 within the sequence are provided in SEQ ID NO: 1-44, 198-238, 349-358, and 399. The cDNA sequences of SEQ ID NO: 1-6, 198-199, 349-352, 354, and 356-358 were determined to have less than 75% identity (determined as described above), to sequences in the EMBL database using the computer algorithms FASTA or BLASTN, as described above. The predicted amino acid sequences of SEQ ID NO: 120-125, 275-276, 373-380,
25 and 382 were determined to have less than 75% identity (determined as described above) to sequences in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above.

Further sequencing of the some of the isolated partial cDNA sequences resulted in the isolation of the full-length cDNA sequences provided in SEQ ID NO: 7-14, 200-231,
30 and 372. The corresponding predicted amino acid sequences are provided in SEQ ID NO: 126-133, 277-308, and 396, respectively. Comparison of the full length cDNA

sequences with those in the EMBL database using the computer algorithm FASTA or BLASTN, as described above, revealed less than 75% identity (determined as described above) to known sequences. Comparison of the predicted amino acid sequences provided in SEQ ID NO: 126-133 and 277-308 with those in the SwissProt database using the
5 computer algorithms FASTX or BLASTP, as described above, revealed less than 75% identity (determined as described above) to known sequences.

Comparison of the predicted amino acid sequences corresponding to the cDNA sequences of SEQ ID NO: 15-23 with those in the EMBL using the computer algorithm FASTA database showed less than 75% identity (determined as described above) to
10 known sequences. These predicted amino acid sequences are provided in SEQ ID NO: 134-142.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of full-length cDNA sequences provided in SEQ ID NO: 24-44 and 232-238. The corresponding predicted amino acid sequences are provided in SEQ ID NO: 143-163
15 and 309-315, respectively. These amino acid sequences were determined to have less than 75% identity, determined as described above to known sequences in the SwissProt database using the computer algorithm FASTX.

Isolated cDNA sequences having less than 75% identity to known expressed sequence tags (ESTs) or to other DNA sequences in the public database, or whose
20 corresponding predicted protein sequence showed less than 75% identity to known protein sequences, were computer analyzed for the presence of transmembrane domains coding for putative membrane-bound molecules. Isolated cDNA sequences that have either one or more transmembrane domain(s) within the sequence are provided in SEQ ID NO: 45-63, 239-253, 359-364, 400-402. The cDNA sequences of SEQ ID NO: 45-48,
25 239-249, 359-361, and 363 were found to have less than 75% identity (determined as described above) to sequences in the EMBL database, using the FASTA or BLASTN computer algorithms. Their predicted amino acid sequences provided in SEQ ID NO: 164-167, 316-326, 383, 385-388 and 407-408 were found to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the FASTX
30 or BLASTP database.

Comparison of the predicted amino acid sequences corresponding to the cDNA sequences of SEQ ID NO: 49-63 and 250-253 with those in the SwissProt database showed less than 75% identity (determined as described above) to known sequences. These predicted amino acid sequences are provided in SEQ ID NO: 168-182 and
5 327-330.

Using automated search programs to screen against sequences coding for molecules reported to be of therapeutic and/or diagnostic use, some of the cDNA sequences isolated as described above in Example 1 were determined to encode predicted protein sequences that appear to be family members of known protein families. A family
10 member is here defined to have at least 25% identity in the translated polypeptide to a known protein or member of a protein family. These cDNA sequences are provided in SEQ ID NO: 64-76, 254-264, 365-369, and 403, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 183-195, 331-341, 389-393 and 409, respectively. The cDNA sequences of SEQ ID NO: 64-68, 254-264, and 365-369 show
15 less than 75% identity (determined as described above) to sequences in the EMBL database using the FASTA or BLASTN computer algorithms. Similarly, the amino acid sequences of SEQ ID NO: 183-195, 331-341, and 389-393 show less than 75% identity to sequences in the SwissProt database.

The likely utility for each of the proteins encoded by the DNA sequences of SEQ
20 ID NO: 64-76, 254-264, 365-369, and 403, based on similarity to known proteins, is provided below:

Table 2

FUNCTIONS OF NOVEL PROTEINS

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS
64 372	183 396	Slit, a secreted molecule required for central nervous system development
65	184	Immunoglobulin receptor family. About 40% of leucocyte membrane polypeptides contain immunoglobulin superfamily domains
66 403	185 409	RIP protein kinase, a serine/threonine kinase that contains a death domain to mediate apoptosis
67	186	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation
68	187	Transforming growth factor alpha, a protein which binds epidermal growth factor receptor and stimulates growth and mobility of keratinocytes
69	188	DRS protein which has a secretion signal component and whose expression is suppressed in cells transformed by oncogenes
70	189	A33 receptor with immunoglobulin-like domains and is expressed in greater than 95% of colon tumors
71	190	Interleukin-12 alpha subunit, component of a cytokine that is important in the immune defense against intracellular pathogens. IL-12 also stimulates proliferation and differentiation of TH1 subset of lymphocytes
72	191	Tumor Necrosis Factor receptor family of proteins that are involved in the proliferation, differentiation and death of many cell types including B and T lymphocytes.
73	192	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
74	193	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors
75	194	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
76	195	Immunoglobulin receptor family
254	331	Receptor with immunoglobulin-like domains and homology to A33 receptor which is expressed in greater than 95% of colon tumors
255	332	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS
256	333	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
257	334	Contains protein kinase and ankyrin domains. Possible role in cellular growth and differentiation.
258	335	Notch family proteins which are receptors involved in cellular differentiation.
259	336	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation.
260	337	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors.
261	338	Immunoglobulin receptor family
262	339	ADP/ATP transporter family member containing a calcium binding site.
263	340	Mouse CXC chemokine family members are regulators of epithelial, lymphoid, myeloid, stromal and neuronal cell migration and cancers, agents for the healing of cancers, neuro-degenerative diseases, wound healing, inflammatory autoimmune diseases like psoriasis, asthma, Crohns disease and as agents for the prevention of HIV-1 of leukocytes
264	341	Nucleotide-sugar transporter family member.
365	389	Transforming growth factor betas (TGF-betas) are secreted covalently linked to latent TGF-beta-binding proteins (LTBPs). LTBPs are deposited in the extracellular matrix and play a role in cell growth or differentiation.
366	390	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
367	391	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
368	392	Cell wall protein precursor. Are involved in cellular growth or differentiation.
369	393	HT protein is a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.

These isolated sequences thus encode proteins that influence the growth, differentiation and activation of several cell types. They may usefully be developed as

agents for the treatment and diagnosis of skin wounds, cancers, growth and developmental defects, and inflammatory disease.

The polynucleotide sequences of SEQ ID NO: 77-117, 265-267, and 404-405 are differentially expressed in either keratinocyte stem cells (KSCL) or in transit amplified cells (TRAM) on the basis of the number of times these sequences exclusively appear in either one of the above two libraries; more than 9 times in one and none in the other (Audic S. and Claverie J-M, *Genome Research*, 7:986-995, 1997). The sequences of SEQ ID NO: 77-89, 265-267, and 365-369 were determined to have less than 75% identity to sequences in the EMBL and SwissProt databases using the computer algorithm FASTA or BLASTN, as described above. The proteins encoded by these polynucleotide sequences have utility as markers for identification and isolation of these cell types, and antibodies against these proteins may be usefully employed in the isolation and enrichment of these cells from complex mixtures of cells. Isolated polynucleotides and their corresponding proteins exclusive to the stem cell population can be used as drug targets to cause alterations in regulation of growth and differentiation of skin cells, or in gene targeting to transport specific therapeutic molecules to skin stem cells.

Example 3

ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF MUTR1

The human homolog of muTR1 (SEQ ID NO: 68), obtained as described above in Example 1, was isolated by screening 50,000 pfu's of an oligo dT primed HeLa cell cDNA library. Plaque lifts, hybridization, and screening were performed using standard molecular biology techniques (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). The determined cDNA sequence of the isolated human homolog (huTR1) is provided in SEQ ID NO: 118, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 196. The library was screened using an $[\alpha \text{ } ^{32}\text{P}]$ -dCTP labeled double stranded cDNA probe corresponding to nucleotides 1 to 459 of the coding region within SEQ ID NO: 118.

The polypeptide sequence of huTR1 has regions similar to Transforming Growth Factor-alpha, indicating that this protein functions like an epidermal growth factor (EGF).

This EGF-like protein will serve to stimulate keratinocyte growth and motility, and to inhibit the growth of epithelial-derived cancer cells. This novel gene and its encoded protein may thus be used as agents for the healing of wounds and regulators of epithelial-derived cancers.

5 Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for huTR1 was performed by probing human tissue mRNA blots (Clontech) with a probe comprising nucleotides 93-673 of SEQ ID NO: 118, radioactively labeled with [$\alpha^{32}\text{P}$]-dCTP. 10 Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huTR1 was 3.5-4kb in size and was observed to be most abundant in heart and placenta, with expression at lower levels being observed in spleen, thymus prostate and ovary (Fig. 1).

The high abundance of mRNA for huTR1 in the heart and placenta indicates a 15 role for huTR1 in the formation or maintenance of blood vessels, as heart and placental tissues have an increased abundance of blood vessels, and therefore endothelial cells, compared to other tissues in the body. This, in turn, demonstrates a role for huTR1 in angiogenesis and vascularization of tumors. This is supported by the ability of Transforming Growth Factor-alpha and EGF to induce *de novo* development of blood 20 vessels (Schreiber, *et al.*, *Science* 232:1250-1253, 1986) and stimulate DNA synthesis in endothelial cells (Schreiber, *et al.*, *Science* 232:1250-1253, 1986), and their over-expression in a variety of human tumors.

Purification of muTR1 and huTR1

Polynucleotides 177-329 of muTR1 (SEQ ID NO: 268), encoding amino acids 25 53-103 of muTR1 (SEQ ID NO: 342), and polynucleotides 208-360 of huTR1 (SEQ ID NO: 269), encoding amino acids 54-104 of huTR1 (SEQ ID NO: 343), were cloned into the bacterial expression vector pProEX HT (BRL Life Technologies), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook *et al.*, *Ibid.*

30 Starter cultures of these recombinant XL1-Blue *E. coli* were grown overnight at 37°C in Terrific broth containing 100 µg/ml ampicillin. This culture was spun down and

used to inoculate 500 ml culture of Terrific broth containing 100 µg/ml ampicillin. Cultures were grown until the OD₅₉₅ of the cells was between 0.4 and 0.8, whereupon IPTG was added to 1 mM. Cells were induced overnight and bacteria were harvested by centrifugation.

5 Both the polypeptide of muTR1 (SEQ ID NO: 342; referred to as muTR1a) and that of huTR1 (SEQ ID NO: 343; referred to as huTR1a) were expressed in insoluble inclusion bodies. In order to purify the polypeptides muTR1a and huTR1a, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM beta mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP40 was added and the mix
10 incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at 95W for 4 x 15 seconds and then centrifuged for 15 minutes at 14,000 rpm to pellet the inclusion bodies.

The resulting pellet was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated on ice for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged
15 at 14,000 rpm for 15 minutes at 4 °C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M Guanidine HCl, 0.5 M NaCl, 20 mM Tris HCl, pH 8.0), sonicated at 95 W for 4 x 15 seconds and then centrifuged for 20 minutes at 14,000 rpm and 4 °C to remove
20 debris. The supernatant was stored at 4 °C until use.

Polypeptides muTR1a and huTR1a were purified by virtue of the N-terminal 6x Histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating Sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's recommended protocol. In order to refold the proteins once purified, the
25 protein solution was added to 5x its volume of refolding buffer (1 mM EDTA, 1.25 mM reduced glutathione, 0.25 mM oxidised glutathione, 20 mM Tris-HCl, pH 8.0) over a period of 1 hour at 4 °C. The refolding buffer was stirred rapidly during this time, and stirring continued at 4 °C overnight. The refolded proteins were then concentrated by ultrafiltration using standard protocols.

Biological Activities of Polypeptides muTR1a and huTR1a

muTR1 and huTR1 are novel members of the EGF family, which includes EGF, TGF α , epiregulin and others. These growth factors are known to act as ligands for the EGF receptor. The pathway of EGF receptor activation is well documented. Upon
5 binding of a ligand to the EGF receptor, a cascade of events follows, including the phosphorylation of proteins known as MAP kinases. The phosphorylation of MAP kinase can thus be used as a marker of EGF receptor activation. Monoclonal antibodies exist which recognize the phosphorylated forms of 2 MAP kinase proteins – ERK1 and ERK2.

10 In order to examine whether purified polypeptides of muTR1a and huTR1a act as a ligand for the EGF receptor, cells from the human epidermal carcinoma cell line A431 (American Type Culture Collection, No. CRL-1555, Manassas, Virginia) were seeded into 6 well plates, serum starved for 24 hours, and then stimulated with purified muTR1a or huTR1a for 5 minutes in serum free conditions. As a positive control, cells were
15 stimulated in the same way with 10 to 100 ng/ml TGF- α or EGF. As a negative control, cells were stimulated with PBS containing varying amounts of LPS. Cells were immediately lysed and protein concentration of the lysates estimated by Bradford assay. 15 μ g of protein from each sample was loaded onto 12% SDS-PAGE gels. The proteins were then transferred to PVDF membrane using standard techniques.

20 For Western blotting, membranes were incubated in blocking buffer (10mM Tris-HCl, pH 7.6, 100 mM NaCl, 0.1% Tween-20, 5% non-fat milk) for 1 hour at room temperature. Rabbit anti-Active MAP kinase pAb (Promega, Madison, Wisconsin) was added to 50 ng/ml in blocking buffer and incubated overnight at 4 °C. Membranes were washed for 30 mins in blocking buffer minus non-fat milk before being incubated with
25 anti rabbit IgG-HRP antibody, at a 1:3500 dilution in blocking buffer, for 1 hour at room temperature. Membranes were washed for 30 minutes in blocking buffer minus non-fat milk, then once for 5 minutes in blocking buffer minus non-fat milk and 0.1% Tween-20. Membranes were then exposed to ECL reagents for 2 min, and then autoradiographed for 5 to 30 min.

30 As shown in Fig. 2, both muTR1a and huTR1a were found to induce the phosphorylation of ERK1 and ERK2 over background levels, indicating that muTR1 and

huTR1 act as ligands for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor. As shown in Fig. 11, huTR1a was also demonstrated to induce the phosphorylation of ERK1 and ERK2 in CV1/EBNA kidney epithelial cells in culture, as compared with the negative control. These assays were
5 conducted as described above. This indicates that huTR1a acts as a ligand for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor in HeLa and CV1/EBNA cells.

The ability of muTR1a to stimulate the growth of neonatal foreskin (NF) keratinocytes was determined as follows. NF keratinocytes derived from surgical
10 discards were cultured in KSFM (BRL Life Technologies) supplemented with bovine pituitary extract (BPE) and epidermal growth factor (EGF). The assay was performed in 96 well flat-bottomed plates in 0.1 ml unsupplemented KSFM. MuTR1a, human transforming growth factor alpha (huTGF α) or PBS-BSA was titrated into the plates and 1×10^3 NF keratinocytes were added to each well. The plates were incubated for 5 days
15 in an atmosphere of 5% CO₂ at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 3, both muTR1a and the positive control human TGF α stimulated the growth of NF keratinocytes, whereas the negative control, PBS-BSA, did not.

The ability of muTR1a and huTR1a to stimulate the growth of a transformed
20 human keratinocyte cell line, HaCaT, was determined as follows. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (BRL Life Technologies) supplemented with 0.2% FCS. MuTR1a, huTR1a and PBS-BSA were titrated into the plates and 1×10^3 HaCaT cells were added to each well. The plates were incubated for 5 days in an atmosphere containing 10% CO₂ at 37°C. The degree of cell growth was
25 determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 4, both muTR1a and huTR1a stimulated the growth of HaCaT cells, whereas the negative control PBS-BSA did not.

The ability of muTR1a and huTR1a to inhibit the growth of A431 cells was determined as follows. Polypeptides muTR1a (SEQ ID NO: 342) and huTR1a (SEQ ID
30 NO: 343) and PBS-BSA were titrated as described previously (*J. Cell. Biol.* 93:1-4, 1982) and cell death determined using the MTT dye reduction as described previously

(*J. Imm. Meth.* 93:157-165, 1986). Both muTR1a and huTR1a were found to inhibit the growth of A431 cells, whereas the negative control PBS-BSA did not (Fig. 5).

These results indicate that muTR1 and huTR1 stimulate keratinocyte growth and motility, inhibit the growth of epithelial-derived cancer cells, and play a role in angiogenesis and vascularization of tumors. This novel gene and its encoded protein may thus be developed as agents for the healing of wounds, angiogenesis and regulators of epithelial-derived cancers.

Upregulation of huTR1 and mRNA expression

HeLa cells (human cervical adenocarcinoma) were seeded in 10 cm dishes at a concentration of 1×10^6 cells per dish. After incubation overnight, media was removed and replaced with media containing 100 ng/ml of muTR1, huTR1, huTGF α , or PBS as a negative control. After 18 hours, media was removed and the cells lysed in 2 ml of TRIzol reagent (Gibco BRL Life Technologies, Gaithersburg, Maryland). Total RNA was isolated according to the manufacturer's instructions. To identify mRNA levels of huTR1 from the cDNA samples, 1 μ l of cDNA was used in a standard PCR reaction. After cycling for 30 cycles, 5 μ l of each PCR reaction was removed and separated on a 1.5% agarose gel. Bands were visualized by ethidium bromide staining. As can be seen from Fig. 12, both mouse and human TR1 up-regulate the mRNA levels of huTR1 as compared with cells stimulated with the negative control of PBS. Furthermore, TGF α can also up-regulate the mRNA levels of huTR1.

These results indicate that TR1 is able to sustain its own mRNA expression and subsequent protein expression, and thus is expected to be able to contribute to the progression of diseases such as psoriasis where high levels of cytokine expression are involved in the pathology of the disease. Furthermore, since TGF α can up-regulate the expression of huTR1, the up-regulation of TR1 mRNA may be critical to the mode of action of TGF α .

Serum response element reporter gene assay

The serum response element (SRE) is a promoter element required for the regulation of many cellular immediate-early genes by growth. Studies have demonstrated that the activity of the SRE can be regulated by the MAP kinase signaling pathway. Two cell lines, PC12 (rat pheochromocytoma – neural tumor) and HaCaT (human transformed

keratinocytes), containing eight SRE upstream of an SV40 promotor and luciferase reporter gene were developed in-house. 5×10^3 cells were aliquoted per well of 96 well plate and grown for 24 hours in their respective media. HaCaT SRE cells were grown in 5% fetal bovine serum (FBS) in D-MEM supplemented with 2mM L-glutamine (Sigma, St. Louis, Missouri), 1mM sodium pyruvate (BRL Life Technologies), 0.77mM L-asparagine (Sigma), 0.2mM arginine (Sigma), 160mM penicillin G (Sigma), 70mM dihydrostreptomycin (Roche Molecular Biochemicals, Basel, Switzerland), and 0.5 mg/ml geneticin (BRL Life Technologies). PC12 SRE cells were grown in 5% fetal bovine serum in Ham F12 media supplemented with 0.4 mg/ml geneticin (BRL Life Technologies). Media was then changed to 0.1% FBS and incubated for a further 24 hours. Cells were then stimulated with a titration of TR1 from 1 μ g/ml. A single dose of basic fibroblast growth factor at 100 ng/ml (R&D Systems, Minneapolis, Minnesota) or epidermal growth factor at 10 ng/ml (BRL Life Technologies) was used as a positive control. Cells were incubated in the presence of muTR1 or positive control for 6 hours, washed twice in PBS and lysed with 40 μ l of lysis buffer (Promega). 10 μ l was transferred to a 96 well plate and 10 μ l of luciferase substrate (Promega) added by direct injection into each well by a Victor² fluorimeter (Wallac), the plate was shaken and the luminescence for each well read at 3x1 sec Intervals. Fold induction of SRE was calculated using the following equation: Fold induction of SRE = Mean relative luminescence of agonist/Mean relative luminescence of negative control.

As shown in Fig. 13, muTR1 activates the SRE in both PC-12 (Fig. 13a) and HaCaT (Fig. 13b) cells. This indicates that HaCaT and PC-12 cells are able to respond to muTR1 protein and elicit a response. In the case of HaCaT cells, this is a growth response. In the case of PC-12 cells, this may be a growth, a growth inhibition, differentiation, or migration response. Thus, TR1 may be important in the development of neural cells or their differentiation into specific neural subsets. TR1 may also be important in the development and progression of neural tumors.

Inhibition by the EGF receptor assay

The HaCaT growth assay was conducted as previously described, except that modifications were made as follows. Concurrently with the addition of EGF and TR1 to the media, anti-EGF Receptor (EGFR) antibody (Promega, Madison, Wisconsin) or

negative control antibody, mouse IgG (PharMingen, San Diego, California), were added at a concentration of 62.5 ng/ml.

As seen in Fig. 14, an antibody which blocks the function of the EGFR inhibits the mitogenicity of TR1 on HaCaT cells. This indicates that the EGFR is crucial for transmission of the TR1 mitogenic signal on HaCaT cells. TR1 may bind directly to the EGF receptor. TR1 may also bind to any other members of the EGFR family – ErbB-2, -3, and/or -4 – that are capable of heterodimerizing with the EGFR.

Sequence of splice variant of huTR1, huTR1 β

A variant of huTR1 was isolated from the same library as huTR1 (SEQ ID NO: 118), following the same protocols. This sequence is a splice variant of huTR1 and consists of the ORF of huTR1 minus amino acids 87 to 137. This has the effect of deleting the third cysteine residue of the EGF motif and the transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, huTR1 β is a secreted form of huTR1. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined nucleotide sequence of the splice variant of TR1, referred to as huTR1 β , is given in SEQ ID NO: 371 and the corresponding predicted amino acid sequence is SEQ ID NO: 395.

Example 4

IDENTIFICATION, ISOLATION AND CHARACTERIZATION OF DP3

A partial cDNA fragment, referred to as DP3, was identified by differential display RT-PCR (modified from Liang P and Pardee AB, *Science* 257:967-971, 1992) using mRNA from cultured rat dermal papilla and footpad fibroblast cells, isolated by standard cell biology techniques. This double stranded cDNA was labeled with [α ³²P]-dCTP and used to identify a full length DP3 clone by screening 400,000 pfu's of an oligo dT-primed rat dermal papilla cDNA library. The determined full-length cDNA sequence for DP3 is provided in SEQ ID NO: 119, with the corresponding amino acid sequence being provided in SEQ ID NO: 197. Plaque lifts, hybridization and screening were performed using standard molecular biology techniques.

Example 5ISOLATION AND CHARACTERIZATION OF THE
HUMAN HOMOLOG OF muKS15 Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for muKS1 (SEQ ID NO: 263) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [$\alpha^{32}\text{P}$]-dCTP. Prehybridization, hybridization, washing, and probe labeling were performed as
10 described in Sambrook, *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was observed to be most abundant in brain, lung, muscle, and heart. Expression could also be detected in lower intestine, skin, and kidney. No detectable signal was found in testis, spleen, liver, thymus, stomach.

Human homologue of muKS1

15 MuKS1 (SEQ ID NO: 263) was used to search the EMBL database (Release 50, plus updates to June, 1998) to identify human EST homologues. The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified
20 in AA643952 and HS1301003 when translated. Combination of all three ESTs identified huKS1 (SEQ ID NO: 270) and translated polypeptide SEQ ID NO: 344. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

Bacterial expression and purification of muKS1 and huKS1

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 271), encoding amino acids
25 23-99 of polypeptide muKS1 (SEQ ID NO: 345), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 272), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 346), were cloned into the bacterial expression vector pET-16b (Novagen, Madison, Wisconsin), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in
30 Sambrook *et al.*, *Ibid.*

Starter cultures of recombinant BL 21 (DE3) *E. coli* (Novagen) containing SEQ ID NO: 271 (muKS1a) and SEQ ID NO: 272 (huKS1a) were grown in NZY broth containing 100 µg/ml ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 µg/ml ampicillin. Cultures were grown until the OD₅₉₅ of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an induced band of approximately 15kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM βMercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14000 rpm for 15 minutes at 4°C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged, and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95W for 4 x 15 seconds and centrifuged for 10 minutes at 18000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM tris-HCl pH 7.5 + 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 + 10% glycerol.

Peptide sequencing of muKS1 and huKS1

Bacterially expressed muKS1 and huKS1 were separated on polyacrylamide gels and induced bands of 15 kDa were identified. The predicted size of muKS1 is 9.4 kDa.

To obtain the amino acid sequence of the 15 kDa bands, 20 µg recombinant muKS1 and huSK1 was resolved by SDS-PAGE and electroblotted onto Immobilon PVDF membrane (Millipore, Bedford, Massachusetts). Internal amino acid sequencing was performed on tryptic peptides of muKS1 and huKS1 by the Protein Sequencing Unit at the University
5 of Auckland, New Zealand.

The determined amino acid sequences for muKS1 and huKS1 are given in SEQ ID NOS: 397 and 398, respectively. These amino acid sequences confirmed that the determined sequences are identical to that predicted from the cDNA sequences. The size discrepancy has previously been reported for other chemokines (Richmond A,
10 Balentien E, Thomas HG, Flaggs G, Barton DE, Spiess J, Bordoni R, Francke U, Derynck R, "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-thromboglobulin," *EMBO J.* 7:2025-2033, 1988; Liao F, Rabin RL, Yannelli JR, Koniaris LG, Vanguri P, Farber JM, "Human Nig chemokine: biochemical and functional characterization,"
15 *J. Exp. Med.* 182:1301-1314, 1995). The isoelectric focusing point of these proteins was predicted to be 10.26 using DNASIS (HITACHI Software Engineering, San Francisco, California).

Oxidative burst assay

Oxidative burst assays were used to determine responding cell types. 1×10^7
20 PBMC cells were resuspended in 5 ml HBSS, 20mM HEPES, 0.5% BSA and incubated for 30 minutes at 37°C with 5 µl 5 mM dichloro-dihydrofluorescein diacetate (H₂DCFDA, Molecular Probes, Eugene, Oregon). 2×10^5 H₂DCFDA-labeled cells were loaded in each well of a flat-bottomed 96 well plate. 10 µl of each agonist was added simultaneously into the well of the flat-bottomed plate to give final concentrations of
25 100 ng/ml (fMLP was used at 10 µM). The plate was then read on a Victor² 1420 multilabel counter (Wallac, Turku, Finland) with a 485 nm excitation wavelength and 535 nm emission wavelength. Relative fluorescence was measured at 5 minute intervals over 60 minutes.

A pronounced respiratory burst was identified in PBMC with a 2.5 fold difference
30 between control treated cells (TR1) and cells treated with 100 ng/ml muKS1 (Fig. 8).

Human stromal derived factor-1 α (SDF1 α) (100 ng/ml) and 10 μ M formyl-Met-Leu-Phe (fMLP) were used as positive controls.

Chemotaxis assay

Cell migration in response to muKS1 was tested using a 48 well Boyden's chamber (Neuro Probe Inc., Cabin John, Maryland) as described in the manufacturer's protocol. In brief, agonists were diluted in HBSS, 20mM HEPES, 0.5% BSA and added to the bottom wells of the chemotactic chamber. THP-1 cells were re-suspended in the same buffer at 3×10^5 cells per 50 μ l. Top and bottom wells were separated by a PVP-free polycarbonate filter with a 5 μ m pore size for monocytes or 3 μ m pore size for lymphocytes. Cells were added to the top well and the chamber incubated for 2 hours for monocytes and 4 hours for lymphocytes in a 5% CO₂ humidified incubator at 37°C. After incubation, the filter was fixed and cells scraped from the upper surface. The filter was then stained with Diff-Quick (Dade International Inc., Miami, Florida) and the number of migrating cells counted in five randomly selected high power fields. The results are expressed as a migration index (the number of test migrated cells divided by the number of control migrated cells).

Using this assay, muKS1 was tested against T cells and THP-1 cells. MuKS1 induced a titrateable chemotactic effect on THP-1 cells from 0.01 ng/ml to 100 ng/ml (Fig. 9). Human SDF1 α was used as a positive control and gave an equivalent migration. MuKS1 was also tested against IL-2 activated T cells. However, no migration was evidence for muKS1 even at high concentrations, whereas SDF-1 α provided an obvious titrateable chemotactic stimulus. Therefore, muKS1 appears to be chemotactic for THP-1 cells but not for IL-2 activated T cells at the concentrations tested.

Full length sequence of muKS1 clone

The nucleotide sequence of muKS1 was extended by determining the base sequence of additional ESTs. Combination of all the ESTs identified the full-length muKS1 (SEQ ID NO: 370) and the corresponding translated polypeptide sequence in SEQ ID NO: 394.

Analysis of human RNA transcripts by Northern blotting

Northern blot analysis to determine the size and distribution of mRNA for the human homologue of muKS1 was performed by probing human tissue blots (Clontech,

Palo Alto, California) with a radioactively labeled probe consisting of nucleotides 1 to 288 of huKS1 (SEQ ID NO: 270). Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huKS1 was 1.6 kb in size and was observed to be most abundance in kidney, liver, colon, small intestine, and spleen. Expression could also be detected in pancreas, skeletal muscle, placenta, brain, heart, prostate, and thymus. No detectable signal was found in lung, ovary, and testis.

Analysis of human RNA transcripts in tumor tissue by Northern blotting

Northern blot analysis to determine distribution of huKS1 in cancer tissue was performed as described previously by probing tumor panel blots (Invitrogen, Carlsbad, California). These blots make a direct comparison between normal and tumor tissue. MRNA was observed in normal uterine and cervical tissue but not in the respective tumor tissue. In contrast, expression was up-regulated in breast tumor and down-regulated in normal breast tissue. No detectable signal was found in either ovary or ovarian tumors.

15 *Injection of bacterially expressed muKS1a into nude mice*

Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20ug of bacterially expressed muKS1a (SEQ ID NO: 345) was injected subcutaneously in the left hind foot, ear and left-hand side of the back. The same volume of phosphate buffered saline was injected in the same sites but on the right-hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline. Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

Injection of bacterially recombinant muKS1 into C3H/HeJ mice

30 Eighteen C3H/HeJ mice were divided into 3 groups and injected intraperitoneally with muKS1, GV14B, or phosphate buffered saline (PBS). GV14B is a bacterially

expressed recombinant protein used as a negative control. Group 1 mice were injected with 50 µg of muKS1 in 1 ml of PBS; Group 2 mice were injected with 50 µg of GV14B in 1 ml of PBS; and Group 3 mice with 1 ml of PBS. After 18 hours, the cells in the peritoneal cavity of the mice were isolated by intraperitoneal lavage with 2 x 4 ml washes
5 with harvest solution (0.02% EDTA in PBS). Viable cells were counted from individual mice from each group. Mice injected with 50 µg of muKS1 had on average a 3-fold increase in cell numbers (Fig. 10).

20 µg of bacterial recombinant muKS1 was injected subcutaneously into the left hind foot of three C3H/HeJ mice. The same volume of PBS was injected into the same
10 site on the right-hand side of the same animal. After 18 hours, mice were examined for inflammation. All mice showed a red swelling in the foot pad injected with bacterially recombinant KS1. From histology, sites injected with muKS1 had an inflammatory response of a mixed phenotype with mononuclear and polymorphonuclear cells present.

Chemokines are a large superfamily of highly basic secreted proteins with a broad
15 number of functions (Baggiolini, *et al.*, *Annu. Rev. Immunol.*, 15:675-705, 1997; Ward, *et al.*, *Immunity*, 9:1-11, 1998; Horuk, *Nature*, 393:524-525, 1998). The polypeptide sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore be expected to stimulate
20 leukocyte, epithelial, stromal, and neuronal cell migration; promote angiogenesis and vascular development; promote neuronal patterning, hemopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes; and promotion of migration in wound healing events. It has recently been shown that receptors to chemokines act as co-receptors for HIV-1 infection
25 of CD4+ cells (Cairns, *et al.*, *Nature Medicine*, 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury, *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid, stromal, and neuronal cells migration and cancers; as agents for the
30 treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases

such as psoriasis, asthma and Crohn's disease for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

We have also shown that muKS1 can promote a quantifiable increase in cell numbers in the peritoneal cavity of C3H/HeJ mice injected with muKS1. Furthermore, we have shown that muKS1 can induce an oxidative burst in human peripheral blood mononuclear cells and migration in the human monocyte leukemia cell line, THP-1, suggesting that monocyte/macrophages are one of the responsive cell types for KS1. In addition to this, we demonstrated that huKS1 was expressed at high levels in a number of non-lymphoid tissues, such as the colon and small intestine, and in breast tumors. It was also expressed in normal uterine and cervical tissue, but was completely down-regulated in their respective tumors. It has recently been shown that non-ELR chemokines have demonstrated angiostatic properties. IP-10 and Mig, two non-ELR chemokines, have previously been shown to be up-regulated during regression of tumors (Tannenbaum CS, Tubbs R, Armstrong D, Finke JH, Bukowski RM, Hamilton TA, "The CXC Chemokines IP-10 and Mig are necessary for IL-12-mediated regression of the mouse RENCA tumor," *J. Immunol.* 161: 927-932, 1998), with levels of expression inversely correlating with tumor size (Kanegane C, Sgadari C, Kanegane H, Teruya-Feldstine J, Yao O, Gupta G, Farber JM, Liao F, Liu L, Tosato G, "Contribution of the CXC Chemokines IP-10 and Mig to the antitumor effects of IL-12," *J. Leuko. Biol.* 64: 384-392, 1998). Furthermore, neutralizing antibodies to IP-10 and Mig would reduce the anti-tumor effect, indicating the contribution these molecules make to the anti-tumor effects. Therefore, it is expected that in the case of cervical and uterine tumors, KS1 would have similar properties.

The data demonstrates that KS1 is involved in cell migration showing that one of the responsive cell types is monocyte/macrophage. The human expression data in conjunction with the *in vitro* and *in vivo* biology demonstrates that this molecule may be a useful regulator in cell migration, and as an agent for the treatment of inflammatory diseases, such as Crohn's disease, ulcerative colitis, and rheumatoid arthritis; and cancers, such as cervical adenocarcinoma, uterine leiomyoma, and breast invasive ductal carcinoma.

Example 6CHARACTERIZATION OF KS2

KS2 contains a transmembrane domain and may function as either a membrane-bound ligand or a receptor. Northern analysis indicated that the mRNA for KS2 was expressed in the mouse keratinocyte cell line, Pam212, consistent with the cDNA being identified in mouse keratinocytes.

Mammalian Expression

To express KS2, the extracellular domain was fused to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This was performed by cloning polynucleotides 20-664 of KS2 (SEQ ID NO: 273), encoding amino acids 1-215 of polypeptide KS2 (SEQ ID NO: 347), into the mammalian expression vector pcDNA3 (Invitrogen, NV Leek, Netherlands), to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This construct was transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid*. The Fc fusion construct of KS2a was expressed by transfecting Cos-1 cells in 5 x T175 flasks with 180 µg of KS1a using DEAE-dextran. The supernatant was harvested after seven days and passed over a Ni-NTA column. Bound KS2a was eluted from the column and dialysed against PBS.

The ability of the Fc fusion polypeptide of KS2a to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes was determined as follows. A single cell suspension was prepared from the spleens of BALB/c mice and washed into DMEM (GIBCO-BRL) supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 0.77 mM L-asparagine, 0.2 mM L-arginine, 160 mM penicillin G, 70 mM dihydrostreptomycin sulfate, 5×10^{-2} mM beta mercaptoethanol and 5% FCS (cDMEM). Splenocytes (4×10^6 /ml) were stimulated with 2 µg/ml concanavalin A for 24 hrs at 37°C in 10% CO₂. The cells were harvested from the culture, washed 3 times in cDMEM and resuspended in cDMEM supplemented with 10 ng/ml rhuIL-2 at 1×10^5 cells/ml. The assay was performed in 96 well round bottomed plates in 0.2 ml cDMEM. The Fc fusion polypeptide of KS2a, PBS, LPS and BSA were titrated into the plates and 1×10^4 activated T cells (0.1 ml) were added to each well. The plates were incubated for 2 days in an atmosphere containing 10% CO₂ at 37°C. The degree of proliferation was

determined by pulsing the cells with 0.25 uCi/ml tritiated thymidine for the final 4 hrs of culture after which the cells were harvested onto glass fiber filtermats and the degree of thymidine incorporation determined by standard liquid scintillation techniques. As shown in Fig. 6, the Fc fusion polypeptide of KS2a was found to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes, whereas the negative controls PBS, BSA and LPS did not.

This data demonstrates that KS2 is expressed in skin keratinocytes and inhibits the growth of cytokine induced splenocytes. This suggests a role for KS2 in the regulation of skin inflammation and malignancy.

10

Example 7

Characterization of KS3

KS3 encodes a polypeptide of 40 amino acids (SEQ ID NO: 129). KS3 contains a signal sequence of 23 amino acids that would result in a mature polypeptide of 17 amino acids (SEQ ID NO: 348; referred to as KS3a).

KS3a was prepared synthetically (Chiron Technologies, Victoria, Australia) and observed to enhance transferrin-induced growth of the rat intestinal epithelial cells IEC-18 cells. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (GIBCO-BRL Life Technologies) supplemented with 0.2% FCS. KS3a (SEQ ID NO: 348), apo-Transferrin, media and PBS-BSA were titrated either alone, with 750 ng/ml Apo-transferrin or with 750 ng/ml BSA, into the plates and 1×10^3 IEC-18 cells were added to each well. The plates were incubated for 5 days at 37°C in an atmosphere containing 10% CO_2 . The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 7, KS3a plus Apo-transferrin was found to enhance transferrin-induced growth of IEC-18 cells, whereas KS3a alone or PBS-BSA did not, indicating that KS3a and Apo-transferrin act synergistically to induce the growth of IEC-18 cells.

This data indicates that KS3 is epithelial derived and stimulates the growth of epithelial cells of the intestine. This suggests a role for KS3 in wound healing, protection from radiation- or drug-induced intestinal disease, and integrity of the epithelium of the intestine.

SEQ ID NOS: 1-409 are set out in the attached Sequence Listing. The codes for polynucleotide and polypeptide sequences used in the attached Sequence Listing confirm to WIPO Standard ST.25 (1988), Appendix 2.

5 All references cited herein, including patent references and non-patent references, are hereby incorporated by reference in their entireties.

Although the present invention has been described in terms of specific embodiments, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

10

We claim:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (1) the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (2) complements of the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (3) reverse complements of the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (4) reverse sequences of the sequences recited in SEQ ID NO: 1-119, 198-274, 349-372, and 399-405; (5) sequences having at least a 99% probability of being the same as a sequence selected from any of the sequences in (1)-(4), above, as measured by the computer algorithm BLASTP using the running parameters described above; and (6) nucleotide sequences having at least 50% identity to any of the sequences in (1)-(4), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
2. An expression vector comprising an isolated polynucleotide of claim 1.
3. A host cell transformed with an expression vector of claim 2.
4. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (1) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409; (2) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP using the running parameters described above; and (3) sequences having at least 50% identity to a sequence provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
5. An isolated polynucleotide encoding a polypeptide of claim 4.
6. An expression vector comprising an isolated polynucleotide of claim 5.

7. A host cell transformed with an expression vector of claim 6.
8. An isolated polypeptide comprising at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of:
5 (1) sequences provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409;
(2) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP using the running parameters described above; and (3) sequences
10 having at least 50% identity to a sequence provided in SEQ ID NO: 120-197, 275-348, 373-398, and 406-409, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.
9. A method for stimulating keratinocyte growth and motility in a patient, comprising administering to the patient a composition comprising an isolated
15 polypeptide, the polypeptide comprising an amino acid sequence of claim 4.
10. The method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397 and 398; (2) sequences having at least about 50% identity to a
20 sequence of SEQ ID NO: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.
11. A method for inhibiting the growth of cancer cells in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the
25 polypeptide comprising an amino acid sequence of claim 4.
12. The method of claim 11, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a
30 sequence of SEQ ID NO: 187, 196, 342, 343, 397, and 398, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

13. A method for modulating angiogenesis in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

5

14. A method of claim 13, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 187, 196, 342, 343, 397 and 398 as measured by the computer
10 algorithm BLASTP, using the running parameters and identity test defined above.

15. A method for inhibiting angiogenesis and vascularization of tumors in a patient, comprising administering to a patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

15

16. The method of claim 15, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 342, 343, 397, and 398; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 187, 196, 340, 342-346, 397, and 398, as measured by the
20 computer algorithm BLASTP, using the running parameters and identity test defined above.

17. A method for modulating skin inflammation in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the
25 polypeptide comprising an amino acid sequence of claim 4.

18. The method of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 338 and 347; and (2) sequences having at least 50% identity to a sequence of SEQ ID
30 NO: 338 and 347 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

19. A method for stimulating the growth of epithelial cells in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

5

20. The method of claim 19, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 129 and 348; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 129 and 348 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

10

21. A method for inhibiting the binding of HIV-1 to leukocytes in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

15

22. A method of claim 21, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 340, 344, 345 and 346; (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 340, 344, 345 and 346 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

20

23. A method for treating an inflammatory disease in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

25

24. The method of claim 23, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 340, 344, 345 and 346; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 340, 344, 345 and 346 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

30

25. A method for treating cancer in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

5 26. The method of claim 25, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 340, 344, 345 and 346; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 340, 344, 345 and 346 as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

10

27. A method for treating neurological disease in a patient, comprising administering to the patient a composition comprising an isolated polypeptide, the polypeptide comprising an amino acid sequence of claim 4.

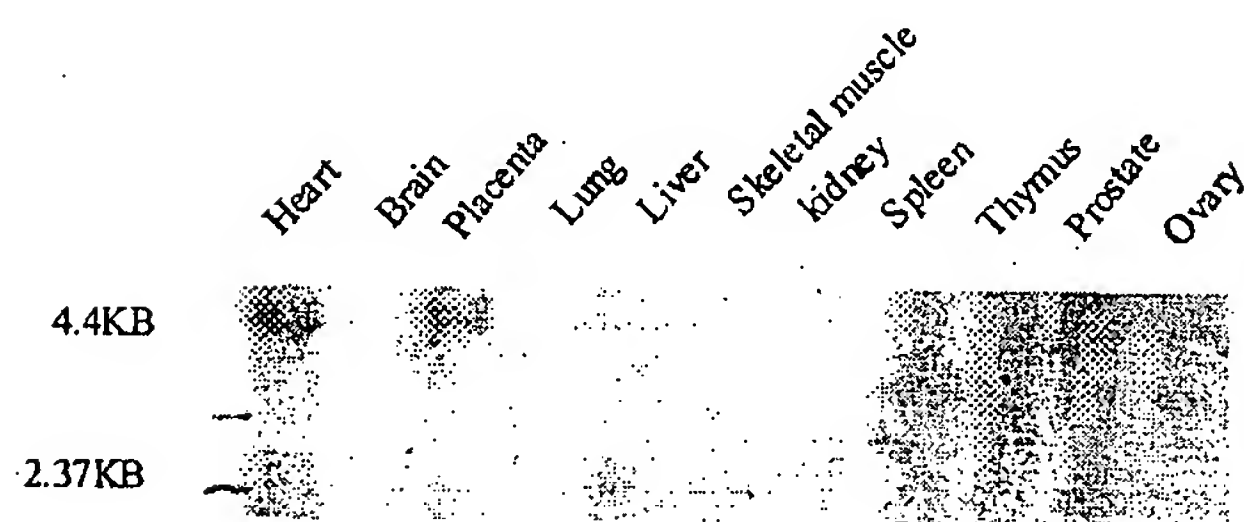
15 28. The method of claim 27, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (1) a sequence provided in SEQ ID NO: 187, 196, 340, 342-346, and 395; and (2) sequences having at least 50% identity to a sequence of SEQ ID NO: 187, 196, 340, 342-346, and 395, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

20

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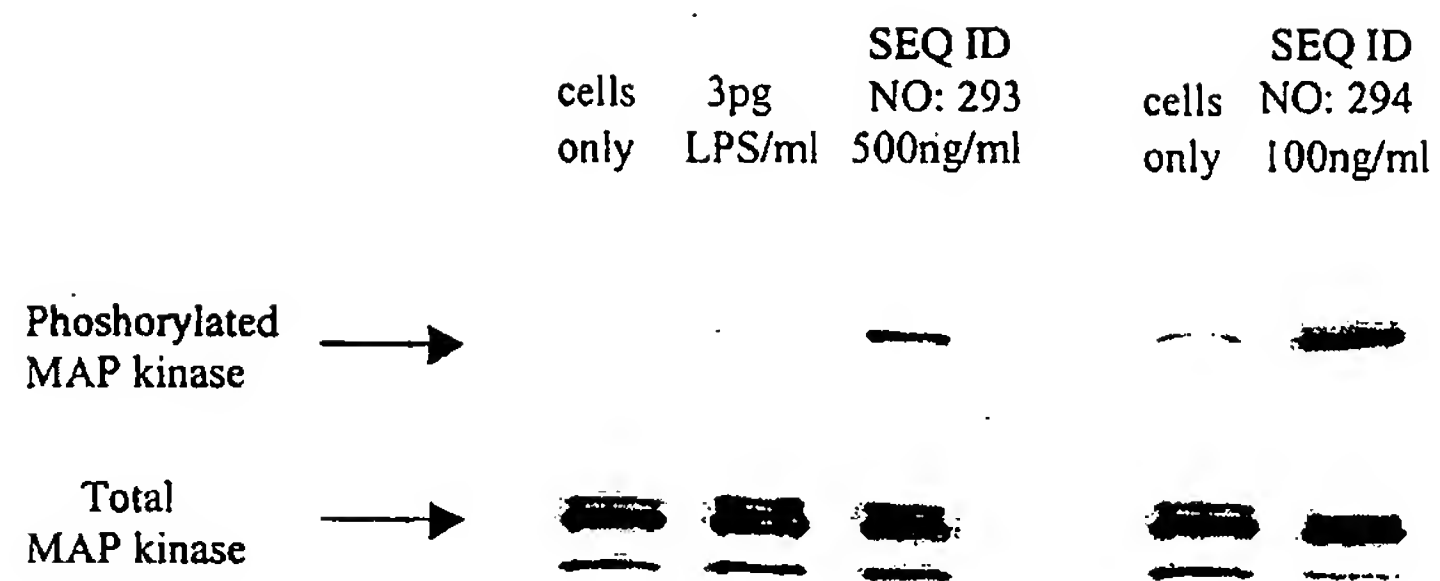
Figure 1

Distribution of human TAK1 mRNA in human tissues

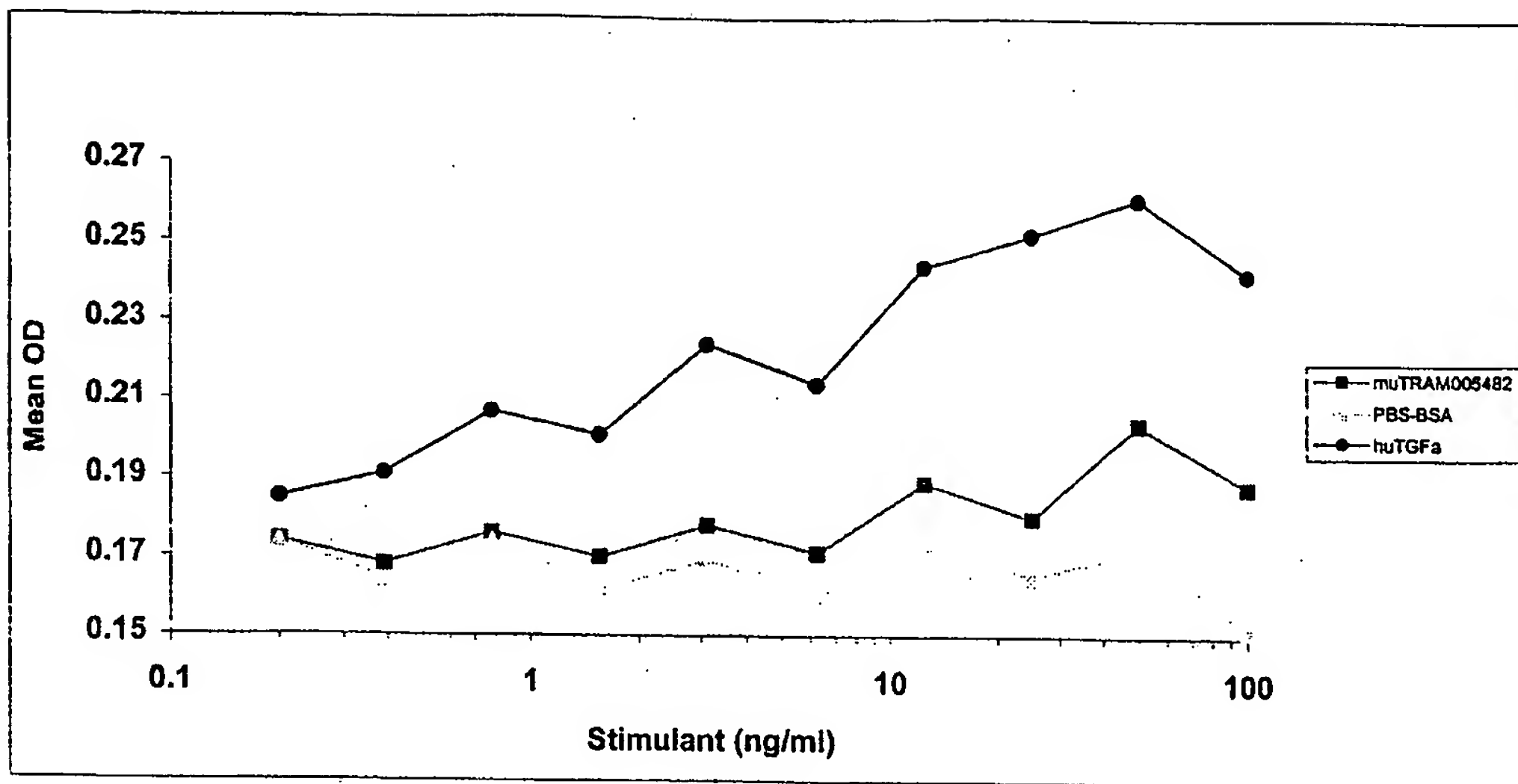


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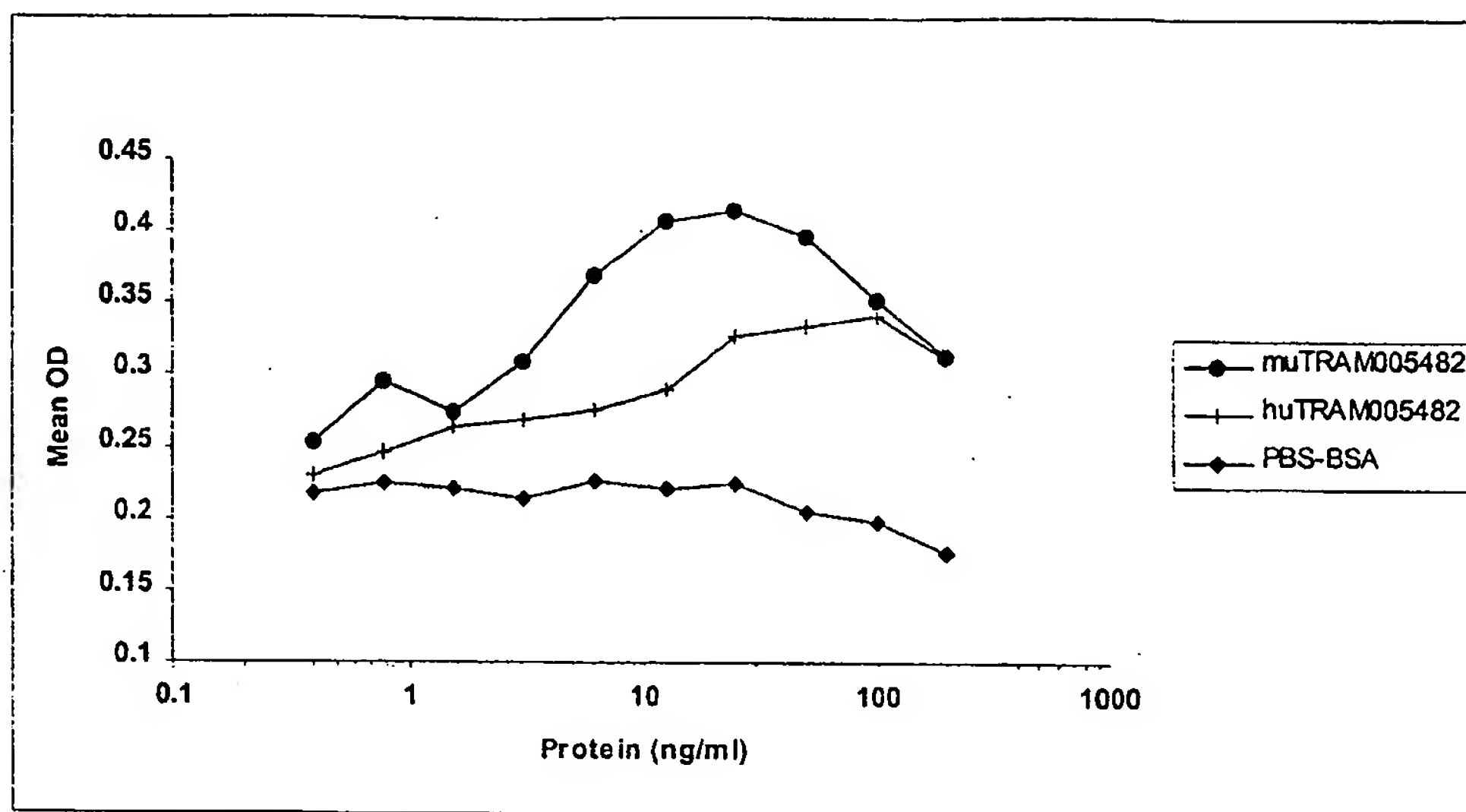
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Figure 2



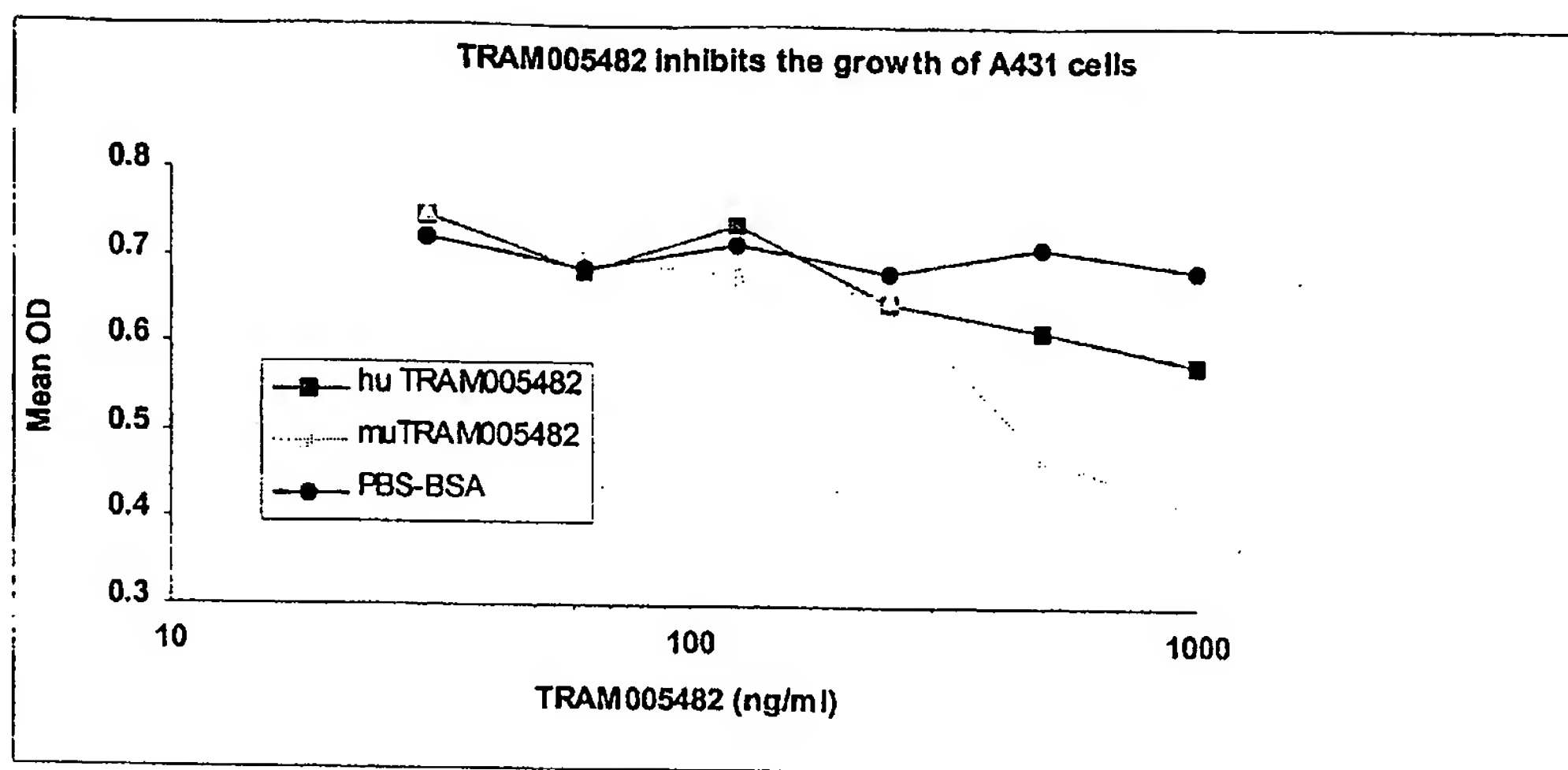
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3/14
Figure 3

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4/14
Figure 4

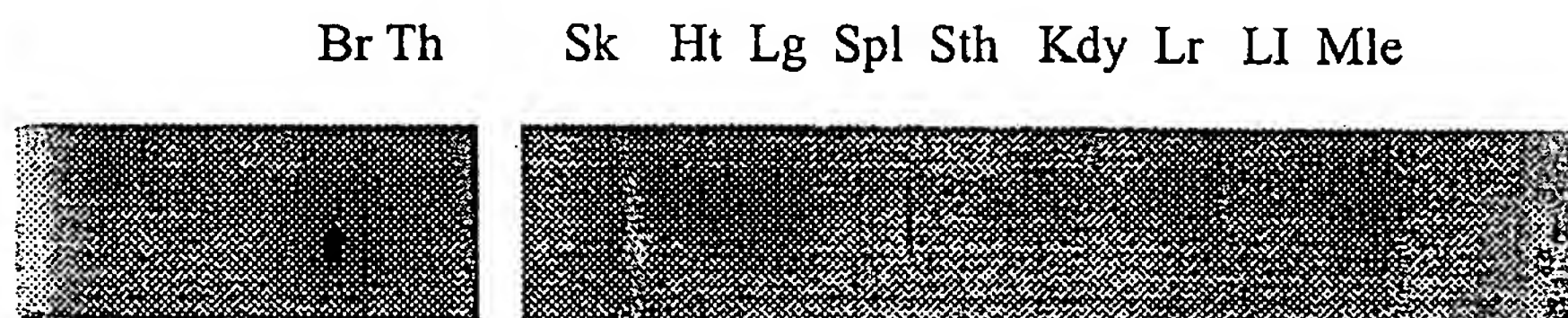
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Figure 5

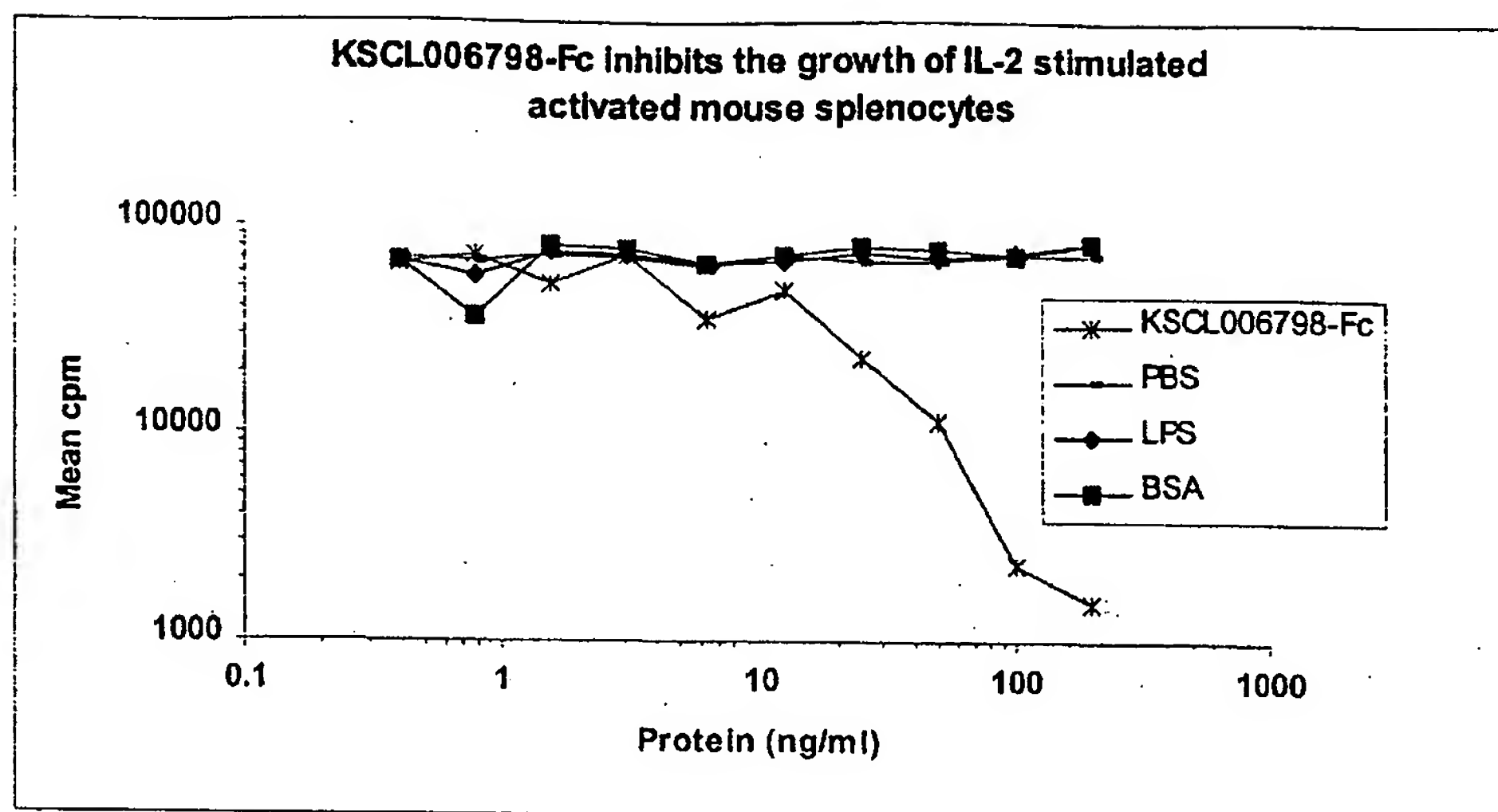
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Figure 6

Key: Br, Brain; Th, Thymus; Sk, Skin; Ht, Heart; Lg, Lung; Spl, Spleen; Sth, Stomach; Kdy, Kidney; Lr, Liver; LI, Lower intestine; Ts, Testis; Mle, Muscle.



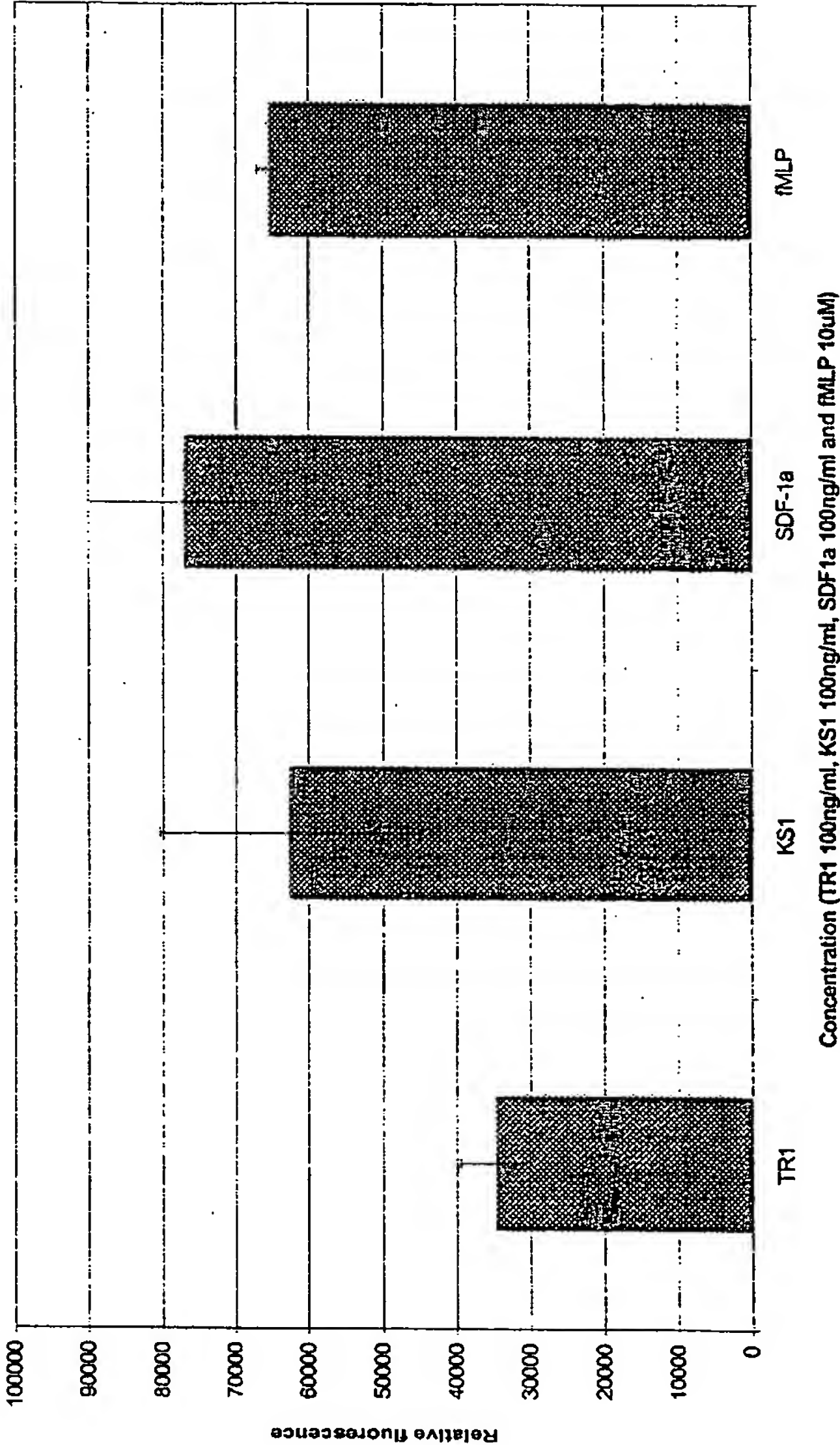
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Figure 7

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Figure 8

KS1 Induces an oxidative burst in human peripheral blood mononuclear cells

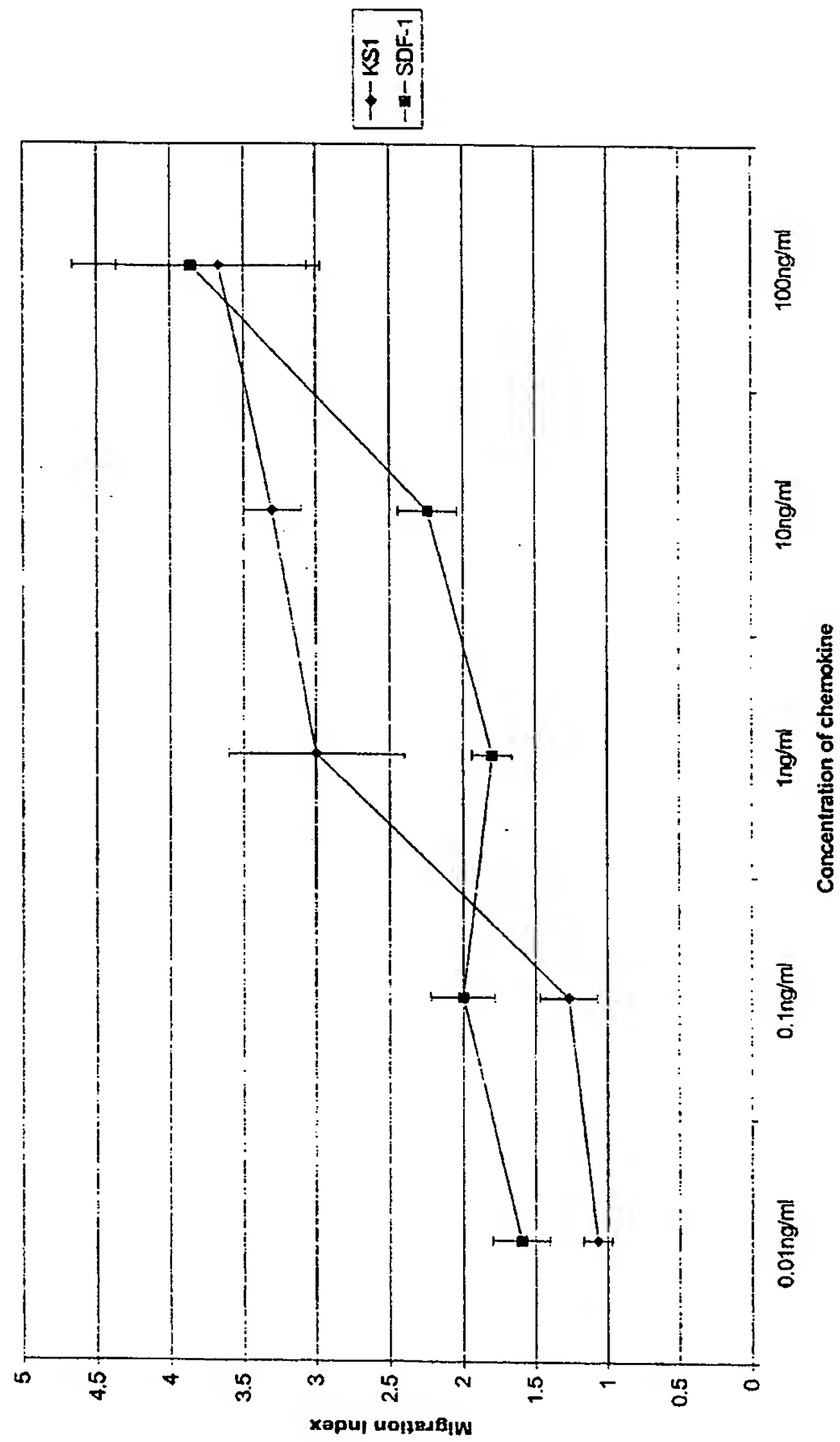


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Figure 9

KS1 stimulates migration of THP-1 cells, a monocyte/macrophage cell line

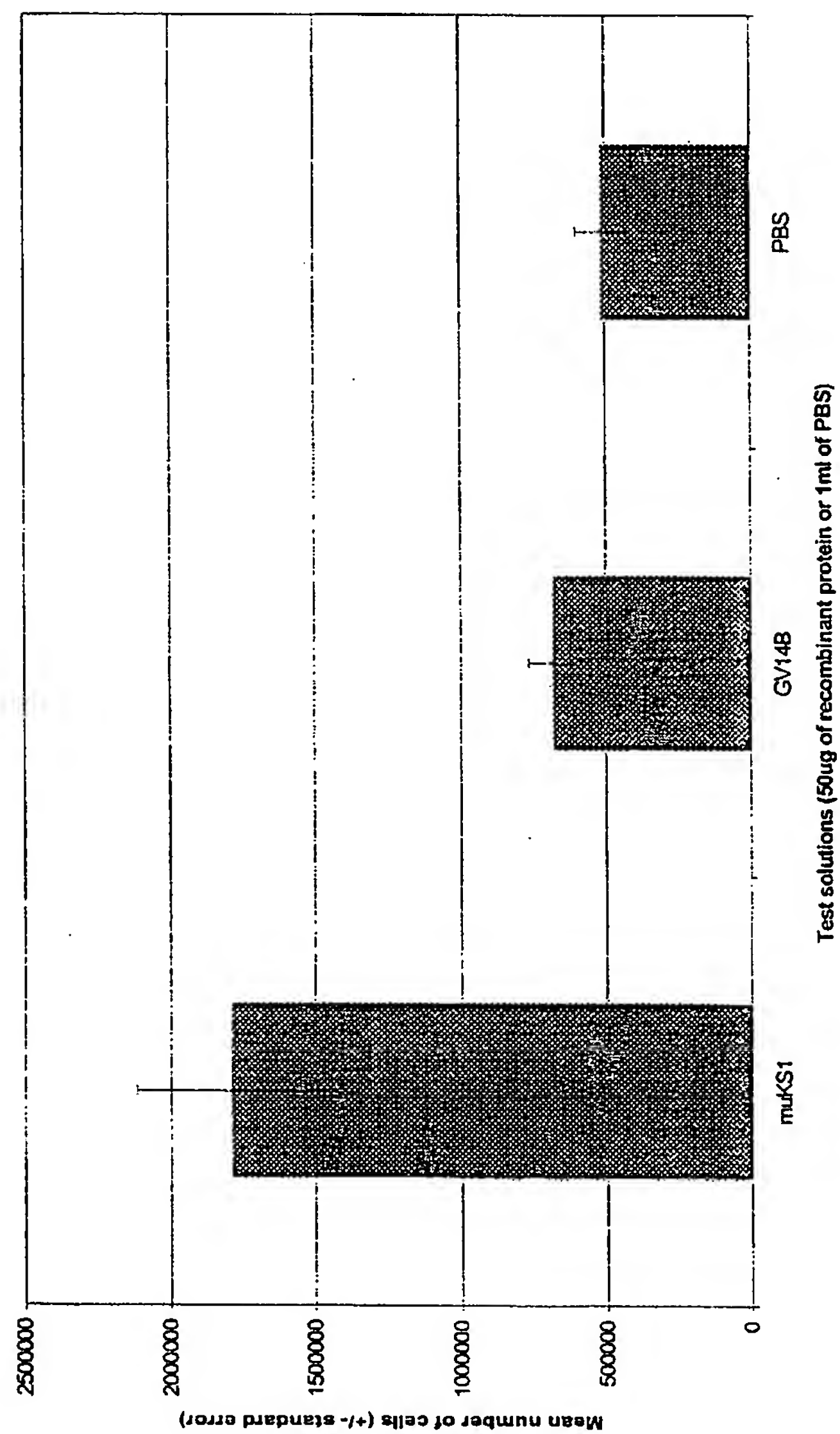


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Figure 10

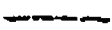

IP injection of muKS1 induces a cellular infiltrate in C3/HeJ mice



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Figure 11

Cell Line	Cells stimulated with		
	PBS	Hu TR1	
CV1/EBNA			← ERK1/2
HeLa			← ERK1/2

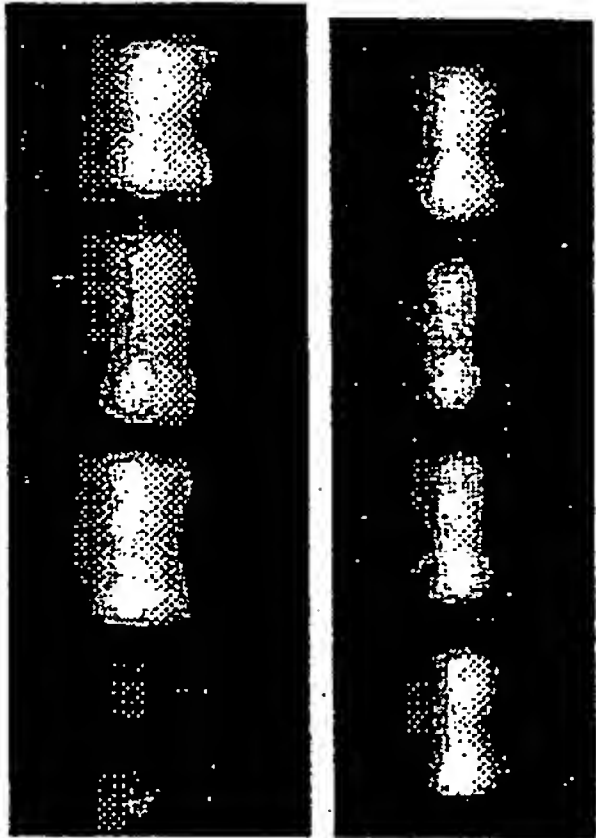
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Figure 12

mu and huTR1 upregulate huTR1 mRNA expression in HeLa cells

HeLa cells stimulated with

PBS muTR1 huTR1 huTGFα



huTR1 mRNA

Actin mRNA

Figure 13A

Murine Tr1 activates the SRE reporter in PC12SRE cells

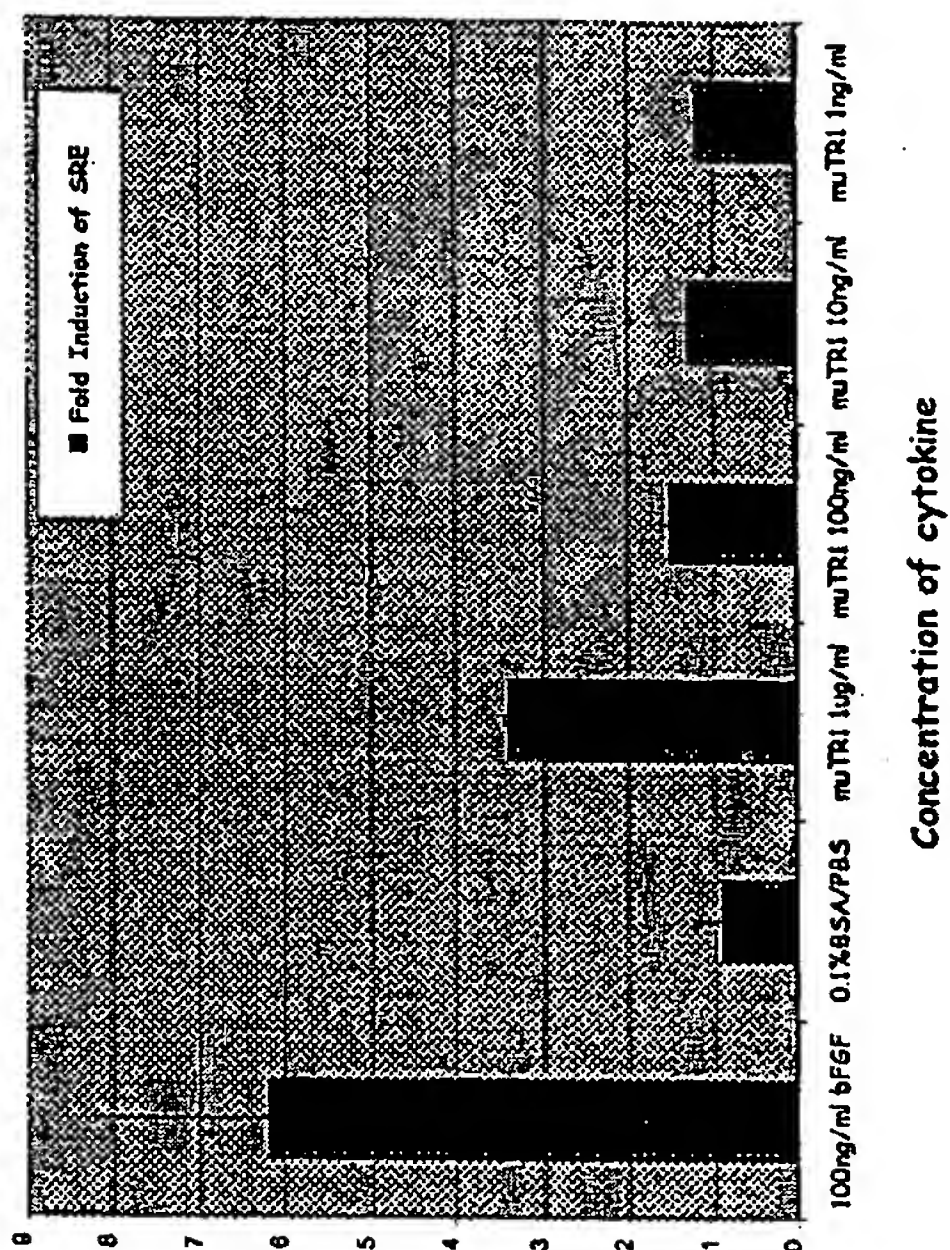
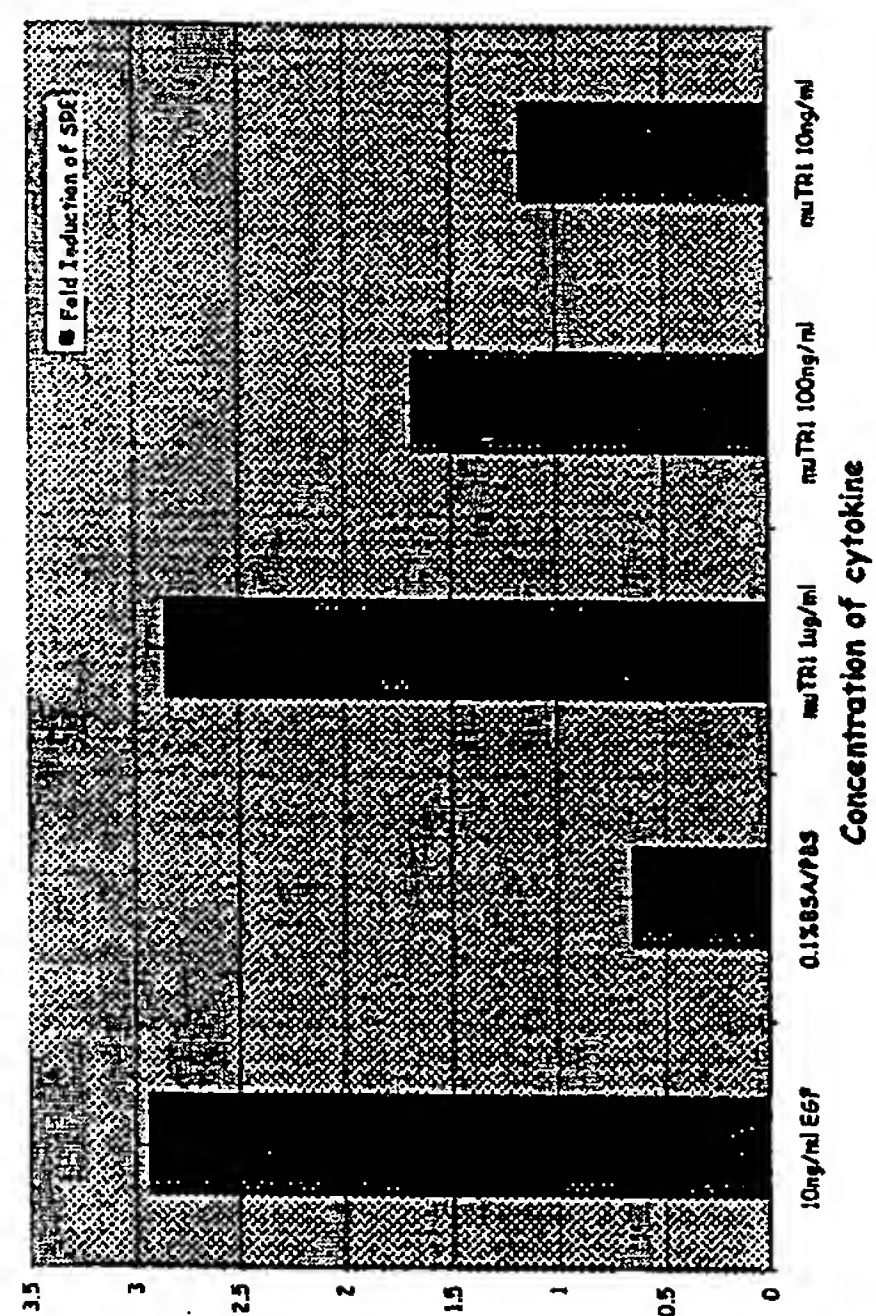


Figure 13B

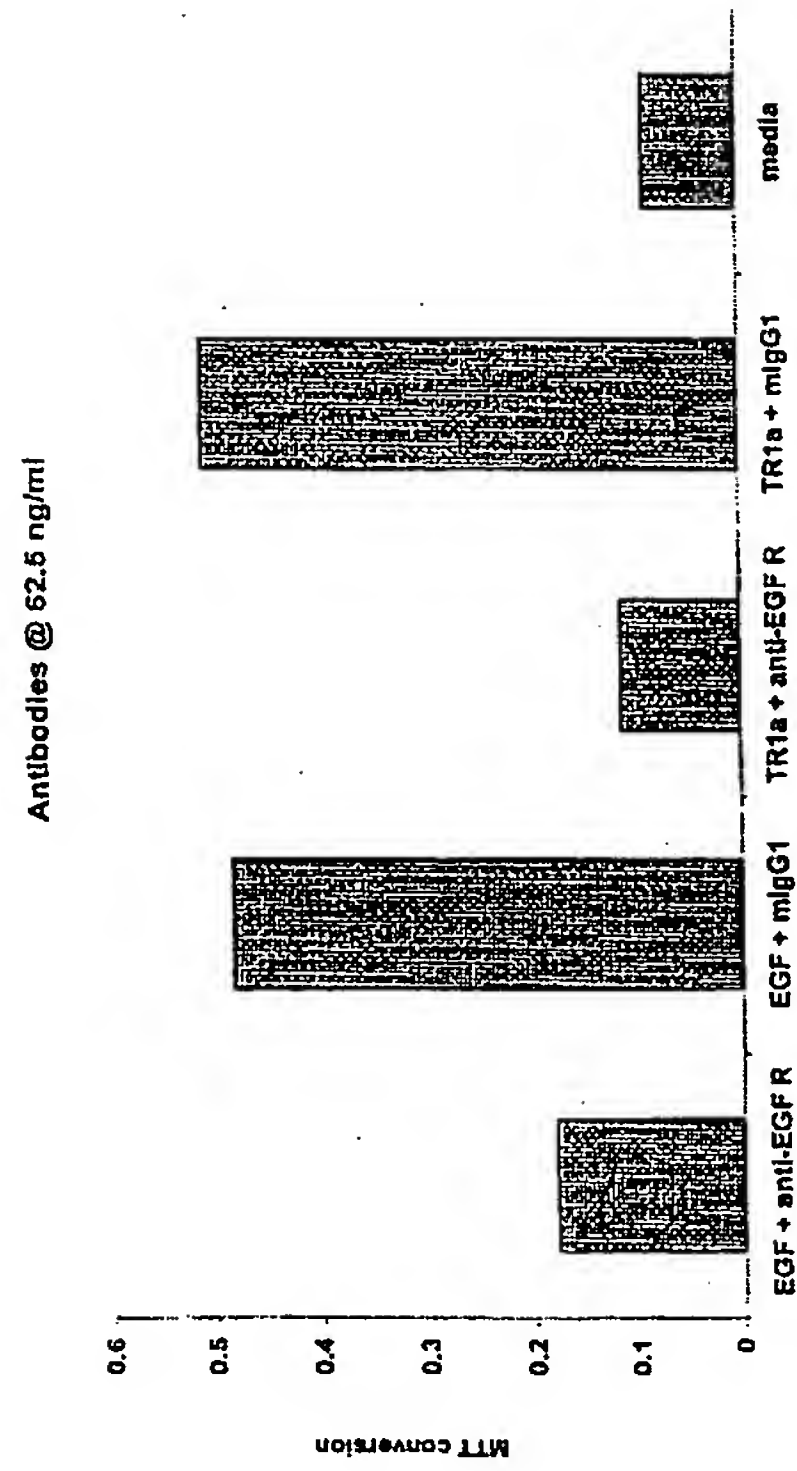
Murine Tr1 activates the SRE reporter in HaCatSRE cells



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Figure 14

TR1 growth of HaCat cells is inhibited by an antibody to the EGF receptor



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SEQUENCE LISTING

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Watson, James D.
 Strachan, Lorna
 Sleeman, Matthew
 Onrust, Rene
 Murison, James Greg
 Kumble, Anand

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<210> 13
 <211> 888
 <212> DNA
 <213> mouse

<400> 13

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<210> 14
 <211> 547
 <212> DNA
 <213> mouse

<400> 14

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<210> 15
 <211> 318
 <212> DNA
 <213> Rat

<400> 15

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<210> 16
 <211> 856
 <212> DNA
 <213> Rat

<400> 16						
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<210> 17
 <211> 349
 <212> DNA
 <213> Rat

<400> 17						
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<210> 18
 <211> 1057
 <212> DNA
 <213> Rat

<220>

<400> 18						
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<210> 19
 <211> 750
 <212> DNA
 <213> Rat

<400> 19

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<210> 20
 <211> 849
 <212> DNA
 <213> Rat

<400> 20

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 <211> 312
 <212> DNA
 <213> Human

<400> 21

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312

<210> 22
 <211> 1023
 <212> DNA
 <213> mouse

<400> 22

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<210> 23
 <211> 997
 <212> DNA
 <213> mouse

<400> 23

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<210> 24
 <211> 529
 <212> DNA
 <213> Rat

<400> 24

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<210> 25
 <211> 1230
 <212> DNA
 <213> Rat

<400> 25

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aagtacactt	tctgcagctg	gcgcccgcga	ggctgctacc	gagctgcgcg	ctcttccagg	1140
acctcatccg	ctacgggaag	accaagcagt	ccggctcgcg	gcgcccgcgc	gtctgcagcc	1200
cgggggatcc	actagttcta	gagcgccgcc				1230

<210> 26
 <211> 393
 <212> DNA
 <213> Rat

<400> 26

ggcagcaaga	agcaaccgcg	aagctaggag	tctgtcagcg	agggcagggg	ctgcctgggt	60
ggggtaggag	tgggagcagg	gccagcagga	gggtctgagg	aagccattca	aagcgagcag	120
ctgggagagc	tgggagcccg	ggaaggccct	acagactaca	agagaggatc	ctggcgctcg	180
ggcctcctgg	gtcatcacca	tgaggccact	tcttgccctg	ctgcttctgg	gtctggcatc	240
aggctctcct	cctctggacg	acaacaagat	ccccagcctg	tgccccgggc	agccccgcct	300
cccaggcaca	ccaggccacc	acggcagcca	aggcctgcct	ggccgtgacg	gcctgatggc	360
cgcgacgggtg	caccgggagt	ccgggagaga	aac			393

<210> 27
 <211> 778
 <212> DNA
 <213> Rat

<400> 27

ctgcaggtcg	acactagtgg	atccaaagat	tcggcacgag	ataaggcaca	tttgcttcat	60
aaaataaaaa	aaaaggaaat	ttacttagcc	gcatgtcagt	cacccaaatt	ttgagtgtac	120
aaatgaaatg	gaaaacattt	attacacaaa	tttaattaca	attctaggga	ataaacatgc	180
aaatcagatg	gagctcaatc	tgcaggcgct	gatcctctcc	ccctgggttg	cagtctgtgc	240
acctcctgga	ttcgcccgcg	accaggcagt	cagaggcctg	gctcttgacg	gcaggaggat	300
cactgttgta	aagaacagcg	tcacatttag	cgcactctgg	gtagtagcag	tttttaacac	360
tttgcgaggg	tgcttccctt	ccccaccgcg	cgctttgtta	ggtctacctc	tctaaatctc	420

tgcccttcctc	gcacagtaag	tgacctctcc	atgacaaaagg	gccccagac	agcagttata	480
aatcaatgtg	ttttgggttt	gtttgtttgt	ttgtttttgt	ttaaagaaaa	acccggccat	540
gcttggtggc	acttgccctt	aatagtagcg	cttggttagac	agaggcaagc	ggttctctgt	600
aagttcaagg	ccagcctggg	ctacacagtg	agaccgggtc	tcaaaaacaa	aacaacaaaa	660
aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	gatcactgtc	tgcaaaactaa	720
agtgacttga	gctcctgtca	cagcctttcc	agcaagggca	agcttcttta	ttagttat	778

<210> 28

<211> 1123

<212> DNA

<213> Rat

<400> 28

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ctagtggatc	caaagaattc	ggcacgagcc	tgaggcgact	acgggtgcggg	tgccgggtgc	120
cgggtgccta	cagcccccat	cagcttcccc	ggggagattc	tgccgatttg	tcacgagcca	180
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agtgttgcca	tggagattat	ggattccgtg	gttaccaagg	gccccctgga	cccccaggtc	360
ctcctggcat	tccaggaaac	catggaaaca	atggaaataa	cggagccact	ggccacgaag	420
gggccaaagg	tgagaaagga	gacaaaggcg	acctggggcc	tcgaggggaa	cgggggcagc	480
atggccccaa	aggatagaag	ggatacccag	gggtgccacc	agagctgcag	attgcgttca	540
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taactgttac	attggtcaca	ctgctactca	ttctaattggc	ataccaatta	tggtggatac	1080
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<210> 29

<211> 849

<212> DNA

<213> Rat

<400> 29

aattcggcac	gaggtgccct	ccgccgggtc	gggatggagc	tgccctgccgt	gaacttgaag	60
gttattctcc	tggttcactg	gctgttgaca	acctggggct	gcttggegtt	ctcaggctcc	120
tatgcttggg	gcaacttcac	tatcctggcc	ctgggtgctg	tggtgtgtgg	cccagcggga	180
ctctgttgat	gccattggca	tgtttcttgg	tggtctgggt	gccaccatct	tcctggacat	240
tatctacatt	agcatcttct	actcaagcgt	tgccgttggtg	gacactggcc	gcttcagtgc	300
cggcatggcc	atcttcagct	tgctgctgca	agcccttctc	ctgctgctc	gtctaccaca	360
tgacccgggc	agcgaggggg	tgagctcccc	ctccgctcgg	atttcttcgg	accttctcag	420
gaacatagtg	cctaccagac	aattgactcg	tcagactcac	ctgcagaccc	ccttgcaagc	480
ctggagaaca	agggccaaagc	tgcccccccg	gggtactgaa	gctgtccctg	gccgtcctgg	540
ggcccagcag	gatgcttgct	accttcttta	ctggacctac	aatgggggat	cctccattcc	600
ctgccacaga	ggtggcctga	gtcatgtgcc	ctcggaggtc	ccagctgaga	agagcccagt	660
cctaattctc	catgctgccc	ctccattcaa	gacacctgtt	aaccctggg	ctagaactgt	720
ggttggtttc	ttccccctct	ccccatcact	ataacacaca	accgccgagc	tgtgcagagt	780
gttcaggggc	atccaggcct	tatggggcaa	tgatcactgc	ctctcaggct	accccaagg	840
gaccagcc						849

<210> 30

<211> 1015

<212> DNA

<213> Rat

<220>

<400> 30

gaattcggca	cgagggagca	agaagcaacc	cgaagctagg	agtctgtcag	cgagggcagg	60
ggctgcctgg	ttggggtagg	agtgggagca	gggccagcag	gagggctctga	ggaagccatt	120
caaagcgagc	agctgggaga	gctggggagc	cggggaagggc	ctacagacta	caagagagga	180
tcctggcgtc	tgggcctcct	gggtcatcac	catgaggcca	cttcttgccc	tgctgcttct	240
gggtctggca	tcaggctctc	ctcctctgga	cgacaacaag	atccccagcc	tgtgtcccgg	300
gcagcccggc	ctcccaggca	caccaggcca	ccacggcagc	caaggcctgc	ctggccgtga	360
cggccgtgat	ggccgcgacg	gtgcacccgg	agctccggga	gagaaaggcg	agggcgggag	420
accgggacta	cctggggccac	gtggggagcc	cgggccgcgt	ggagaggcag	gacctgtggg	480
ggctatcggg	cctgcggggg	agtgtctggg	gccccacga	tcagccttca	gtgccaagcg	540
atcagagagc	cgggtacctc	cgccagccga	cacaccctta	cccttcgacc	gtgtgctgct	600
caatgagcag	ggacattacg	atgccactac	cggcaagtcc	acctgccaaag	tgcttgggtg	660
ctactacttt	gctgtccatg	ccactgtcta	ccgggccagc	ctacagtttg	atcttgtcaa	720
aaatggccaa	tccatagctt	ctttcttcca	gttttttggg	gggtggccaa	agccagcctc	780
gctctcaggg	ggtgcgatgg	tgaggctaga	acctgaggac	caggtatggg	ttcaggtggg	840
tgtgggtgat	tacattggca	tctatgccag	catcaaaaca	gacagtacct	tctctggatt	900
tctcgtctat	tctgactggc	acagctcccc	agtcttcgct	taaaatacag	tgaacccgga	960
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<210> 31

<211> 452

<212> DNA

<213> Human

<400> 31

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ttgttaggaa	aatgtaggct	accagtagaa	aatgacattc	tctattaata	agatctgagg	120
tgcgacacac	ataattgtcc	caattttttaa	gattgatggg	gagcatgaag	cattttttta	180
atgtgttggc	aggccccatt	aaatgcataa	actgcatagg	actcatgtgg	tctgaatgta	240
ttttagggct	ttctgggaat	tgtcttgaca	gagaacctca	gctggacaaa	gcagccttga	300
tctgagttag	ctaactgaca	caatgaaact	gtcaggcatg	tttctgtctc	tctctctggc	360
tcttttctgc	tttttaacag	gtgtcttcag	tcagggagga	caggttgact	gtggtgagtc	420
caggacacca	aggcctactg	cactcgggaa	cc			452

<210> 32

<211> 434

<212> DNA

<213> mouse

<400> 32

accaccaagc	agatggaatg	ctggcacacc	catgcacctg	catggcgtca	caggtggaag	60
attgttaaaa	aattgacatc	agaaatattt	acagaaatag	atacctgttt	gaataaagtt	120
agagatgaaa	tttttgctaa	acttcaaccg	aagcttagat	gcacattagg	tgacatggaa	180
agtctgtgtg	ttgcacttcc	tgtactgtta	aagcttgaac	cccattgtga	aagcctcttt	240
acatattctt	tttcttggaa	ttttgaatgt	tcccattgtg	gacaccagta	ccaaaacagg	300
tgtgtgaaga	gtctggtcac	ctttaccaat	attgttcctg	agtggcatcc	actcaatgct	360
gccatttttg	gtccatgtaa	cagctgcaac	agtaaatac	aaataagaaa	aatgggtgtg	420
gaaagagcgt	cgcc					434

<210> 33

<211> 903

<212> DNA

<213> mouse

<400> 33

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tttttcccac	ctgctgcctt	cacctgagcc	cagcccagag	ggcagctacg	tgggccagca	180
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aggggtcgac	accagagatg	ctccaagggc	ctgcaccaag	ttgcttttgg	gttttttctg	300
gtatttgtgt	tttctgggat	tttattttta	ttattttttt	taatgtcctt	tcttttgggt	360

atagagaaat	ctctgcaaaa	gactttgctg	accaaccagc	tggagctcaa	ggaatgtggg	420
gtatctgggg	ccacaccatt	acctgtgggc	ttgtctctgg	agccaaaccc	tgcagcctta	480
agagagaggg	gcctgacctg	ctctctttcc	ctccctagct	ccaggcctcc	tctcctgcct	540
cgtcactcct	gtgttctggc	ctcttgagtg	cctttggagg	tgtctctgac	ctgtgaggat	600
cagagacagt	ccccgttttt	aaacttcgac	aattgacttt	tatttccttt	tctaattttt	660
attatttttt	aaaacaacca	ggatgattat	cacatctact	cccccatccg	tccagaaaag	720
ccccaaattg	attccttcag	ggctctggcct	gcccaggctc	tattccacat	gtgcagggtc	780
caacagctta	accctattct	cttcccagtc	atctgctgca	ggtatagctg	tctcatgccc	840
ctgcctgcct	attctggcca	gtaccctaag	ccccaagatc	tccagcccct	gccccagtat	900
cct						903

<210> 34

<211> 1359

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (644) ... (644)

<400> 34

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ttgactgtaa	tcttgctgct	tatatgtaca	tgtgcttata	tccgatccct	ggcaccacgc	120
atcctggaca	gaaataaaac	tggactattg	ggaatatttt	ggaagtgtgc	ccgaattggg	180
gaacgcaaga	gtccttatgt	cgccatatgc	tgtatagtga	tggccttcag	catcctcttc	240
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cctccagaaa	ataatgggaa	gaatgggtta	gccatttgtc	tctgaacatg	gaatgagata	360
aacttcaaga	tgctgttctc	tatttttatg	ctattggacc	aatgagctga	atgaataatt	420
aagatgtaac	agttcaatac	acaggaatgt	gattgtatcc	atcaacctca	gttctctcac	480
tccagtatta	cattctgcaa	atgtcattct	gttgtgtcag	gactgctttt	cataagggtc	540
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gttcttaatg	cagtgtttta	agtctagtgt	atgttctgtc	agcttgaact	ggaatctctc	1080
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aagtacattt	cagctttgac	acagaatgtg	aatagacgaa	tatcaaagga	tacttacaag	1200
tttgatatcca	acatttcttc	aggttcagct	gaaaatcagt	tactgtttca	aaacaaagag	1260
gaattaaatc	ctagctgaaa	actatacata	gcatttatta	attaattact	gggtttaact	1320
gctcttttta	aaagtttgaa	aaaaaaaaaa	aaaaactcg			1359

<210> 35

<211> 797

<212> DNA

<213> mouse

<400> 35

aattcggcac	gaggctagtc	gaatgtccgg	gctgcggacg	ctgctggggc	tggggctgct	60
ggttgceggc	tcgcgcctgc	cacgggtcat	cagccagcag	agtgtgtgtc	gtgcaaggcc	120
catctgggtg	ggaacacagc	gccggggctc	ggagaccatg	gcgggcgctg	cgggtgaagta	180
cttaagtcag	gaggaggctc	aggccgtgga	ccaagagctt	tttaacgagt	atcagttcag	240
cgtggatcaa	ctcatggagc	tggccggggt	gagctgtgcc	acggctattg	ccaaggctta	300
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taacggaggg	gatgggctgg	tctgtgcgcg	acacctcaaa	ctttttgggt	accagccaac	420
tatctattac	cccaaaagac	ctaacaagcc	cctcttctact	gggctagtga	ctcagtgtca	480
gaaaatggac	attcctttcc	ttggtgaaat	gccccagag	gatgggatgt	agagaaggga	540
aaccctagcg	gaatccaacc	agacttactc	atctcactga	cggcacccaa	gaagtctgca	600

actcacttta	ctggccgata	tcattacctt	gggggtcgct	ttgtaccacc	tgctctagag	660
aagaagtacc	agctgaacct	gccatcttac	cctgacacag	agtgtgtcta	ccgtctacag	720
taagggaggt	gggtaggcag	gattctcaat	aaagacttgg	tactttctgt	cttgaaaaaa	780
aaaaaaaaaa	aaactcg					797

<210> 36
 <211> 896
 <212> DNA
 <213> mouse

<400> 36

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agataccatg	cagctccctc	tagcctcgga	tcaccgaagc	aggaagaagg	tcagactgcc	120
cccatcccag	atgttgcttag	tttgtctccc	aatgtgctgg	actttaaaga	cagggaatgg	180
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atgttacttg	gtttaatgaa	ggccccctca	accccaacag	ccctcctgc	tcaggacac	840
agttctcacc	caattacaca	ttaataacac	acaaacagtg	cctagcaatg	ggccag	896

<210> 37
 <211> 501
 <212> DNA
 <213> mouse

<400> 37

ctgcaggtcg	acactagtgg	atccaaagaa	ttcggcacga	gaatcatggc	gccgtcgctg	60
tggaaggggc	ttgtaggtgt	cgggcttttt	gccctagccc	acgtgcctt	ttcagctgcg	120
cagcatcggt	cttatatgcg	actaacagaa	aaggaagatg	aatcattacc	aatagatata	180
gttcttcaga	cacttctggc	ctttgcagtt	acctgttatg	gcatagttca	tatcgcaggg	240
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aatcacccat	cttttttatgt	gtttaaccat	cgtggtcgag	tgctgttccg	gccttcagat	360
gcaacaaatt	cttcaaacct	agatgcattg	tcctctaata	catcgttgaa	gttacgaaag	420
tttgactcac	tgcgccgtta	agctttttac	aaattaaata	acaggacaga	cacagaattg	480
agtattggag	tttggggtgt	a				501

<210> 38
 <211> 766
 <212> DNA
 <213> mouse

<400> 38

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ggcgtactgg	agcgagccga	gcagagcaga	gagaggcgtg	cttgaaaccg	agaaccaagc	120
cgggcggcat	ccccgggccc	ccgcacgcac	aggccggcgc	cctccttgcc	tcctgtctcc	180
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ataagacaaa	ttatatattg	ctatgaagct	cttcttacca	gggtcagttt	ttacatttta	660
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766

<210> 39
<211> 480
<212> DNA
<213> mouse

<400> 39

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cgcctggcct	ggcattatga	atgcagtggg	gtcagtgtgt	ggtggatgtg	tgtactgggt	120
tggctttcct	ttttagtttt	tttacttttt	agtttagttt	gttcttttcc	ttccccaata	180
aatcattctc	acatgcttcc	atgtttgttt	ctgagagggtg	ggggctcaaa	tgtatagaaa	240
gtaggcccca	gtccataagg	aggtgtgaac	acaccccctt	actgcttata	acccatttga	300
caggaacgcc	caggagggga	gggggagggg	aagagggtgag	ttctgcacag	tcggacattt	360
ctgttgcttt	tgcattgtta	atatagacgt	tcctgtcgat	ccttgggaga	tcattggcctt	420
cagatatgca	cacgaccttt	gaattgtgcc	tactaattat	agcaggggac	ttgggtaccc	480

<210> 40
<211> 962
<212> DNA
<213> mouse

<400> 40

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cattcatctc	tctctcatte	ccctgctctg	catcctgatg	agaaactgtt	tggcttttaa	120
aaatgatgcc	acagaaatcc	tttattcaca	tgtgggttaa	cctgtcccgg	cacaccccag	180
cagcaacagc	accctgaatc	aagccaggaa	tggaggcagg	catttcagta	gcactggact	240
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gcccctgccg	gtgcttccca	actggatcgg	aggaggctac	ggaacaaagt	actggagccg	420
gaggagctct	caggagtggc	ggtgtgtcaa	cgacaagacg	cgcacccaga	ggatccagct	480
gcagtgtcag	gacggcagca	cgcgcaccta	caaaatcacc	gtggtcacgg	cgtgcaagtg	540
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aagcccagca	ggctgtcctt	ctctgggact	agcttttctt	ttgcaagtgt	ctcaagatgt	840
aatgagtggg	ttgcagtga	agccaggcat	cctgtagttt	ccatcccctc	ccccatccca	900
gtcatttctt	taaaagcacc	tgatgctgca	ttctgttaca	gtttaaaaaa	aaaaaaaaaa	960
aa						962

<210> 41
<211> 794
<212> DNA
<213> mouse

<400> 41

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ggtgggggaa	acagcgccgg	ggctcggaga	ccatggcggg	cgctgcgggtg	aagtacttaa	180
gtcaggagga	ggctcaggcc	gtggaccaag	agctttttta	cgagtatcag	ttcagcgtgg	240
atcaactcat	ggagctggcc	gggttgagct	gtgccacggc	tattgccaag	gcttatcccc	300
ccacgtctat	gtccaagagt	cccccgactg	tcttggtcat	ctgtggcccc	ggaaataacg	360
gaggggatgg	gctgggtctg	gcgcgacacc	tcaaactttt	tggttaccag	ccaactatct	420
attaccccaa	aagacctaac	aagcccctct	tactgggctt	agtgactcag	tgtcagaaaa	480
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ctttactggc	cgatatcatt	accttggggg	tcgctttgta	ccacctgctc	tagagaagaa	660
gtaccagctg	aacctgccat	cttaccctga	cacagagtgt	gtctaccgtc	tacagtaagg	720
gaggtgggta	ggcaggattc	tcaataaaga	cttgggtactt	tctgtcttga	aaaaaaaaaa	780
aaaaaaaaact	cgag					794

<210> 42
 <211> 1152
 <212> DNA
 <213> mouse

<400> 42

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caggctgggc	cacaggaagc	tgctgactgg	ccacttgaca	ccctccccct	aaagctaata	120
tctgtgacta	tagggaggtt	agcacttttt	ctaattggaa	ttcttctctg	tcctgtggcc	180
ccatccctca	cccgtctctg	gcctggacca	gatacatgca	gcctctttct	ccagcacagc	240
ctttccctga	gcctgaggtt	agggcagagt	ttagaggggt	ggctaagtgt	atgttttcat	300
gtatgcattc	atgcctgtga	gtgtgtggct	tgctgtcgtg	tcctctggga	tcccaagcca	360
cgcggtctt	ccctctgtag	atgggtcctg	ggttctatca	cctgcttatt	tatgtacgag	420
gttggggggg	ggaccaggg	tgggttgatt	gtctctttgt	aaggaagtat	gtgtcggggg	480
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magactgcag	agggagctgc	acttttgttt	tgacaaaaaa	caaaaaacaa	aacaaaacaa	600
aaacaaaaca	aaaataactc	tgaagggcgg	gaggataccc	aagcctgatg	cctgagagga	660
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aatttttttg	agtccgtgcc	tgtgggtggc	agtcctgagc	cttcagctga	agcagtgcct	780
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ccagggactc	ccagggtggg	actgctgtgg	cagtgagctc	agcccgga	gacactgcca	960
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tctcagccta	gcaccacctg	tccccgagtc	ttctcagctt	gcccattcatt	ctcggcgccc	1080
acacaggtga	cagtcccaag	tagataacct	ccatggggaca	agttgggtgt	tgccctaccc	1140
gcctgcccag	cc					1152

<210> 43
 <211> 446
 <212> DNA
 <213> mouse

<400> 43

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tttgtttgtt	aatgtgcact	ggtgttttgc	ctggatgtgt	atacttgtga	agatgtcaga	120
actcctggag	ctggagttag	agacaatggt	gagctgcctt	gtggatgttg	ggaattgaac	180
ccaggctctc	tggagaaata	accagtgcct	ttaaccacta	agccatctca	acagcccaaa	240
attatttttt	taataagttg	cctcgggtcat	gttgtcttaa	tcagagcgat	agaaaagtaa	300
ctaatataga	ttatttatga	attcaggtgg	cttaatggta	tatgcatgaa	ttagtagtaa	360
aacaagaact	agggccagca	agtggcttaa	gggtgcctgc	taaccatctc	agccacctga	420
gttcagtctc	caggaaccac	acagtg				446

<210> 44
 <211> 391
 <212> DNA
 <213> mouse

<400> 44

ggcacgagcc	cacgtctatg	ttcaccttcg	ttgttctgg	aatcaccatc	gtcatctgtc	60
tctgccacgt	ctgctttgga	cacttcaaat	acctcagtgc	ccacaactac	aagattgaac	120
acacagagac	agatgccgtg	agctccagaa	gtaatggacg	gccccccact	gctggcgctg	180
tccccaaatc	tgcgaaatac	atcgctcagg	tgctgcagga	ctcagagggg	gacggggacg	240
gagatggggc	tcctggggagc	tcaggcgatg	agcccccatc	gtcctcctcc	caagacgagg	300
agttgctgat	gcctcctgat	ggcctcacgg	acacagactt	ccagtcatgc	gaggacagcc	360
tcataagaaa	tgagattcac	cagtaagggg	t			391

<210> 45
 <211> 516
 <212> DNA
 <213> Rat

<400> 45

cctcctgtct	ctgctgctac	ttgtgaggcc	tgcgcctgtg	gtggcctact	ctgtgtccct	60
cccggcctcc	ttcctggagg	aagtggcggg	cagtggggaa	gctgagggtt	cttcagcctc	120
ttccccaagc	ctgctgccgc	cccggactcc	agccttcagt	cccacaccag	ggaggacca	180
gcccacagct	ccggtcggcc	ctgtgccacc	caccaacctc	ctggatggga	tcgtggactt	240
cttcgccag	tatgtgatgc	tcattgcggt	gggtgggctcg	ctgacctttc	tcatcatgtt	300
catagtctgc	gcggcactca	tcacgcgcca	gaagcacaag	gccacagcct	actaccgctc	360
ctctttcccc	gaaaagaagt	atgtggacca	gagagaccgg	gctggggggc	cccatgcctt	420
cagcgaggtc	cctgacaggg	cacctgacag	ccggcaggaa	gagggcctgg	acttcttcca	480
gcagctccag	gctgacattc	tggcttgcta	ctcaga			516

<210> 46

<211> 306

<212> DNA

<213> mouse

<400> 46

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agggggatca	gaaatggggt	ctcccatctc	tgggtgtctgc	ccagtccttc	cagggtgggct	180
cttcgtagcc	ctgggggtgga	ttttcctcct	cttccacaga	gatgcttttt	ctctgcatac	240
catgtctgct	ggtttcccaa	aatctcccgc	aaaccacac	cacctccac	tgaggctcag	300
ccccag						306

<210> 47

<211> 439

<212> DNA

<213> mouse

<400> 47

gaaaactcgc	aggacgtca	ctggacagct	tgggcttttt	tcagttgatt	ttatggtttg	60
catctttctc	tttctctttt	tctgtttctt	gttccccctt	ccccttttcc	tggtgagaaa	120
gcacatatta	ctgagccatt	gcaagcaatg	ggaggggtcc	acaatgacac	acacacacac	180
acacacacac	atacacatac	acacaccccc	gagacagtgc	cagagctaac	agcctacatg	240
tgtatttttg	ccaaacttgg	aaaataggtt	tccttcttcg	ttttgcttcc	agccttttat	300
ttgcaagtga	tcttccatgc	agtatgaaac	atgcagacag	cactggagtg	tggaagagt	360
gagcttgccc	cacaagtctc	tcggggatgt	tgtactcttg	tgtgtgttta	cagtatcatg	420
gctgttacat	ctactggtc					439

<210> 48

<211> 159

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (3) ... (3)

<400> 48

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ctctttctct	ttttctgttt	cttgttcccc	tttccccctt	tcctgggtgag	aaagcacata	120
ttactgagcc	attgcaagca	atgggagggg	tccacaatg			159

<210> 49

<211> 465

<212> DNA

<213> Rat

<400> 49

gtgccctccg	ccgggtcggg	atggagctgc	ctgccgtgaa	cttgaagggt	attctcctgg	60
------------	------------	------------	------------	------------	------------	----

ttcactggct	ggtgacaacc	tggggctgct	tggcggttctc	aggctcctat	gcttggggca	120
acttcactat	cctggccctg	ggtgctgtgg	gctgtggccc	agcgggactc	tggtgatgcc	180
attggcatgt	ttcttggtgg	cttggttgcc	accatcttcc	tggacattat	ctacattagc	240
atcttctact	caagcgttgc	cgttggggac	actggccgct	tcagtgccgg	catggccatc	300
ttcagcttgc	tgctgcaagc	ccttctcctg	ctgcctcgtc	taccacatgc	accgggcagc	360
gagggggtga	gctcccgcgc	cgctcggatt	tcttcggacc	ttctcaggaa	catagtgcct	420
accagacaat	tgactcgtca	gactcacctg	cagaccccct	tgcaa		465

<210> 50
 <211> 337
 <212> DNA
 <213> Rat

<220>

<400> 50						
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gnategtcct	cagcgnctgg	ggagtgatca	tggtgataat	gctcgggata	tttttcaatg	120
tccattctgc	tgtggtaatt	tagnatgtcc	ccttcacaga	gaaagatttt	nagaacggcc	180
ctcagaacat	atacaacctg	tacgagcaag	tcagctacaa	ctgtttcatc	gccgcggggc	240
tctacctct	cctcgggggc	ttctccttct	genaagttcg	tctcaataag	cgcaaggaat	300
acatggtgcg	ctagagcgna	gtccnactct	ccccatt			337

<210> 51
 <211> 371
 <212> DNA
 <213> Rat

<220>

<221> unsure
 <222> (80) ... (80)

<221> unsure
 <222> (312) ... (312)

<221> unsure
 <222> (319) ... (319)

<221> unsure
 <222> (353) ... (354)

<400> 51						
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ctgctccctc	ccttccagen	ggcgaattca	gcccgcagag	ctgtggcttt	accggaaccc	120
gtacgtgaag	gcggaatact	tccccaccgg	cccatgttt	gtcattgcct	ttctcacccc	180
actgtccctg	atcttcttct	ccaagtctt	gaggaaagct	gacgccgacc	gacagcgagc	240
aagcctgcct	cgtgcccagc	cttgccctag	cgctaaatgg	tgtctttacc	aacatcataa	300
gactgatagt	gngcaaggnc	acgccccaaat	tgcttctacc	gagtgttccc	cgnnccgggat	360
tgcccattct	t					371

<210> 52
 <211> 228
 <212> DNA
 <213> Rat

<400> 52						
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cgcgctctcc	ctttacgtct	tcaccatcgc	cactgatcct	ttgcgagtca	tcttcctcat	120
cgcgggtgcc	ttcttctggt	tggtgtctct	gctgctttcg	tctgttttct	ggttcctagt	180
gagagtcac	actgacaaca	gagatggacc	agtacagaat	tacctgct		228

<210> 53
 <211> 361
 <212> DNA
 <213> Human

<400> 53
 cgtggacact gctgaggaat gataccgagt ggtaggtcag aagaagatgc tgtgaacacc 60
 aggactttta tcttatgctt gaaaatgccat gatgttgctt gggggacaac ttgtatcttt 120
 ctagcagcag atctgtagtt tgtatagcct caacaacaat tttaaataag atggagaata 180
 aattattgag gggactaggg tatatgcatt tgccttcctc cacccatggt tattaagaat 240
 cattgtgctt aataatacca agactaagca ccataaccaa gaaataactaa tgtaaagatt 300
 gtttcttggt tcaggaatgg ttaattcttc aacgttggtg tgataatgat aacttggttt 360
 g 361

<210> 54
 <211> 403
 <212> DNA
 <213> Human

<220>
 <400> 54
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 ggctgatcgc cgatggggac aaaggcgcaa gtcgagagga aactgttggt tctcttcata 120
 ttggcgatcc tgttgtgctc cctggcattg ggcagtgtta cagtgcactc ttctgaacct 180
 gaagtcagaa ttcctgagaa taatcctgtg aagttgtcct gtgcctactc gggcttttct 240
 tctccccgtg tggagtggaa gtttgaccaa ggagacacca ccagactcgt ttgctataat 300
 aacaagatca cagcttccta tgaggaccgg gtgaccttct tgccaactgg tatcaccttc 360
 aagtcctgta cacgggaaga cactgggaca tacacttgta tgg 403

<210> 55
 <211> 413
 <212> DNA
 <213> Human

<400> 55
 tagcgtgggc gcggccgagg tacgactcgg tgctcgccct gtccgcgggc ttgcaggcca 60
 ctcgagccct aatggtgggc tccctgggtg tgggcttcct ggccatgttt gtggccacga 120
 tgggcatgaa gtgcacgcgc tgtgggggag acgacaaagt gaagaaggcc cgtatagcca 180
 tgggtggagg cataattttc atcgtggcag gtcttgccgc cttggtagct tgctcctggt 240
 atggccatca gattgtcaca gacttttata accctttgat ccctaccaac attaatgatg 300
 agtttggtcc tgccatcttt attggctggg caggggtctgc cctagtcctc ctgggaggtg 360
 cactgtctcc tgttcctgtc ctggggataa gagcagggct gggtagctgc ccg 413

<210> 56
 <211> 452
 <212> DNA
 <213> Human

<400> 56
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 ttgttaggaa aatgtaggct accagtagaa aatgacattc tctattaata agatctgagg 120
 tgcgacacac ataattgtcc caatttttaa gattgatggg gagcatgaag cattttttta 180
 atgtgttggc agggcccat aaatgcataa actgcatagg actcatgtgg tctgaatgta 240
 ttttagggct ttctgggaat tgtcttgaca gagaacctca gctggacaaa gcagccttga 300
 tctgagttag ctaactgaca caatgaaact gtcaggcatg tttctgtctc tctctctggc 360
 tcttttctgc tttttaacag gtgtcttcag tcaggaggga cagggtgact gtggtgagtc 420
 caggacacca aggcctactg cactcgggaa cc 452

<210> 57

<211> 190

<212> DNA

<213> Rat

<220>

<400> 57

ttegcggccc	ngtcgacggc	attggcaaat	agtcaaacct	gggaagtaaa	aagcaaaacc	60
aaaaacaaaa	ccaaagaaac	aaactaaaac	aaaacaagaa	aaaccaacat	ttcttcaatt	120
cagtgtgcaa	catatataaa	acagaaatac	taactctaca	ggcagtatgt	cgacgcggcc	180
gcgtattcgg						190

<210> 58

<211> 413

<212> DNA

<213> mouse

<400> 58

ctgcaacaag	gctgttggtt	cctctccaat	gggctccagt	gaagggctcc	tgggcctggg	60
ccctgggccc	aatggtcaca	gtcacctgct	gaagacccca	ctgggtggcc	agaaacgcag	120
tttttccac	ctgctgccct	cacctgagcc	cagcccagag	ggcagctacg	tgggccagca	180
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aggggtcgac	accagagatg	ctccaagggc	ctgcaccaag	ttgcttttgg	gttttttctg	300
gtattttgtg	tttctgggat	tttattttta	ttattttttt	taatgtcctt	tctttgggta	360
atagagaaat	ctctgcaaaa	gactttgctg	accaaccagc	tggagctcaa	gga	413

<210> 59

<211> 325

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (213) ... (213)

<221> unsure

<222> (223) ... (223)

<221> unsure

<222> (227) ... (227)

<221> unsure

<222> (243) ... (243)

<400> 59

ggtatcaccc	aggcccactt	atccatctac	agcgagtagt	atggcggcct	tccttgtaac	60
aggctttttc	ttttctctct	tcgtggtgct	tgggatggaa	cccagggtct	tgtttaggcc	120
tgacaaggct	ctgcccctga	gctgtgccaa	gccacacctc	ctctgtgtac	aaagctcctt	180
tcttgggtga	ccaacatctt	cctgtctttg	agnaaccagg	ggncagnatg	ggagccaccc	240
agnagttaat	taaaccagg	tcatcgggag	tttgctgaaa	tgtaagcat	actctgttct	300
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<210> 60

<211> 372

<212> DNA

<213> mouse

<400> 60

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ggatctcgat	gtgggttaaca	tgtttgtgat	tgcgggtggg	accctggcca	ttccaatcct	120
ggcattttgt	gcgtctttcc	tcctgtggcc	ttcagcactg	ataagaatct	attattggta	180

ctggcgagg	acactgggca	tgcaagtctg	ctacgcacac	catgaggact	atcagttctg	240
ttactccttc	cggggcaggc	caggacacaa	gccatccatc	cttatgctcc	atggattctc	300
cgcacacaaa	ggacatgtgg	ctcagcgtgg	ccaagttcct	tcccgaaga	acctgcactt	360
tggtgtgtg	ga					372

<210> 61
 <211> 363
 <212> DNA
 <213> mouse

 <220>
 <221> unsure
 <222> (15) ... (15)

<400> 61						
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ccaagagctt	tccaccaaag	aagcccctcc	aagcactgac	catgtctatt	atggaccaca	180
gccccaccac	cggggtggta	acggtcattg	tcattcctcat	cgccatagct	gccctggggg	240
gcttgatcct	gggctgctgg	tgctacctgc	ggctgcagcg	catcagccag	tcagaggatg	300
aggagagcat	cgtgggtgat	ggcgagacaa	aggagccctt	ttactggtgc	agtactctgc	360
taa						363

<210> 62
 <211> 399
 <212> DNA
 <213> mouse

<400> 62						
aagggtcctg	aagtcagttg	ttgcatcaaa	tacttcattt	ttggcttcaa	tgtcatattt	60
tggttttttg	gaataacgtt	tcttggaatc	ggactgtggg	cgtggaatga	aaaagggtgc	120
cttccaaca	tctcgtccat	caccgacctc	ggtggctttg	acccagtgtg	gcttttcctc	180
tgagtggcca	gcccagacct	gagctctgtc	aatgacatcc	aaggagaaaa	tgaggttaat	240
gagagacatt	aattaaacac	tccctcaccc	caccgcacca	aaccagtgtg	gttcttctga	300
tattctggaa	tactctgggc	tatgttttat	gtttatttct	tttttaatcg	gttgtatttt	360
ggtctttttt	tttcttcttc	tttttctttt	gctcccaaa			399

<210> 63
 <211> 399
 <212> DNA
 <213> mouse

<220>

<400> 63						
caaagcccac	tgtaggctcc	gctgaggtag	cgattgctgt	atctctgggc	atctgcatca	60
tagtggtctt	aaccatcctg	ggctactgtt	tcttcaagaa	ccaaagaaag	gaattccaca	120
gtcccctgca	ccaccacact	cccacaccag	ccagctccac	tgtttccacc	acagaggaca	180
cagagcacct	ggtctataat	cacacaaccc	agcctctctg	agcctgggac	tcttgccagt	240
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tcttcctacc	tctttcctgg	gcatacttac	gctgtctcag	aagacagatc	tctgggcctc	360
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<210> 64
 <211> 2481
 <212> DNA
 <213> Rat

<400> 64						
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catttaacac	ttatagactt	aagtaacaac	agaataagca	cccttttcaa	ccaaagcttc	120

agcaacatga	cccaacttct	caccttaatt	ctcagttaca	accgtctgag	atgtatccct	180
ccacggacct	ttgatggatt	gaaatctctt	cgtttactgt	ctctacatgg	aaatgacatt	240
tctgtcgtgc	ctgaagggtgc	ctttggtgac	ctttcagcct	tgtcacactt	agcaattgga	300
gccaaccctc	tttactgtga	ttgtaacatg	cagtggttat	ccgactgggt	gaagtccgaa	360
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 <211> 3008
 <212> DNA
 <213> mouse

<220>

<400> 65

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<210> 66

<211> 1888

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (1690) ... (1690)

<221> unsure

<222> (1755) ... (1755)

<221> unsure

<222> (1864) ... (1864)

<400> 66

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<210> 67
 <211> 1260
 <212> DNA
 <213> Rat

<400> 67

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<210> 68
 <211> 1729
 <212> DNA
 <213> mouse

<400> 68

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<210> 69

<211> 355

<212> DNA

<213> Rat

<400> 69

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<210> 70

<211> 1421

<212> DNA

<213> Human

<400> 70

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<210> 71

<211> 378

<212> DNA

<213> Human

<400> 71

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aaagacatca	gctaagaaag	gaaactgggt	cctacggctt	ggactttcca	accctgacag	180
accgcgaaga	caaaacaact	ggttcttgcc	agcctctaga	gaaatcccag	aacactcagc	240
cctgacacgt	taataccctg	cacagatcag	aggctgctgg	ccacacagac	tcaccaagcc	300
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<210> 72

<211> 267

<212> DNA

<213> mouse

<400> 72

ggggcatggg	ccatgctgta	tggagtctcg	atgctctgtg	tgctggacct	aggtcagccg	60
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actcgctgct	gcagcctgta	tgctccaggc	aaggaggact	gtccaaaaga	aagggtcata	180
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tgccaaccag	gccaaagggg	ggaagtc				267

<210> 73

<211> 1633

<212> DNA

<213> mouse

<220>

<400> 73

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<210> 74

<211> 1252

<212> DNA

<213> mouse

<400> 74

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ataccggatc	agaattcagg	ctatcaatga	aattggagtt	ggaccattta	gtcagttcat	180
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<210> 75

<211> 2411

<212> DNA

<213> mouse

<400> 75

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agagtccttt	ctacggcgac	aagatgaact	tgtattctct	gtgtaagaag	atagagcagt	180
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<210> 76

<211> 1335.

<212> DNA

<213> mouse

<400> 76

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ggtccttgat	aacatctaca	cctccgacat	cttggaatc	agcactatgg	ctaactctct	180
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aacccttatt	cctgagagtt	ctgagaccag	ccagaccata	aacacgactc	caactgtgaa	540
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tttccactgt	gccagacca	gtcggtaggt	tttgaaggaa	gtatatgaaa	actgtgcctc	1260
agaagccaat	gacaggacac	atgacttttt	ttttctaagt	caaataaaca	atatattgaa	1320
caaggaaaaa	aaaaa					1335

<210> 77

<211> 440
 <212> DNA
 <213> mouse

<220>

<400> 77

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tcaggcccct caacctccac atcagaacag gcagagcctg tgggtgtcagc tgttgatcca	180	
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tccgagtaag tcatcaaggc	440	

<210> 78
 <211> 204
 <212> DNA
 <213> mouse

<400> 78

ctccataaaa ttcctcaaaa tctgttcccc cagcagattt cctgtgccat cttgggctcc	60
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atgagaaggc actcactgtg tgcctcctca ggcctggcct ctccctgggtga ttgtcttctt	180
cctctgtgtc ctcttcatcc caat	204

<210> 79
 <211> 300
 <212> DNA
 <213> mouse

<220>

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<400> 79

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aacaccttct tctggcctcc atggcacaca gaacccccca acacatgtc atccactctc	180
aaagagacat acataaaaat aaatatattag gtccctgggtc ctcagagac tagtcttcac	240
aggtcctaaa taaaaacga gcggaccgca aagggtgagg gagtggat gaagaagcta	300

<210> 80
 <211> 214
 <212> DNA
 <213> mouse

<400> 80

cccagaccct gtgtcagcta tcccagcaga aaaagaagat gcggaccctc tcagcaagtc	60
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aggatcagat cttgtgtgac ttctgtcttg gggccagcag agtaagggca gtgaaatcct	180
gtctgacctg catggtgaaa tactgtaagg agca	214

<210> 81
 <211> 152
 <212> DNA
 <213> mouse

<220>

<400> 81

ccccttaact	aaccaggac	cttccactaa	gtggaaggct	ccaccatcca	cagagggggc	60
cagtcatttt	taagcacacg	gaccttttgt	gagacagtcg	tgatcttaac	tgtgggtgtca	120
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<210> 82

<211> 181

<212> DNA

<213> mouse

<220>

<400> 82

tetcatgat	gatgagaagc	tccggaggag	gcaggagaaa	gcagggcccc	gccccctccct	60
gggtctccac	ccaccacgc	ccgctaaggt	cacctgttct	cccatggaga	tgatgaagaa	120
gctcatagct	ggacaaggcc	cggaacctca	gccagtaac	cgacctactt	cccgcctggg	180
a						181

<210> 83

<211> 332

<212> DNA

<213> mouse

<220>

<400> 83

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cagatgacat	tcacgtctac	ttctctctgt	gttgggggta	tgggtctgca	cacctgcca	180
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tatctgcttt	aaagtgcac	ataaacatag	cctcctgacc	atcttccaca	gtgggaccct	300
gatctggcct	ctccctggaa	gaagagagaa	ag			332

<210> 84

<211> 213

<212> DNA

<213> mouse

<400> 84

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acattgttgg	ccgcacagca	acgtgctgga	cacaagcatg	ctctcatccc	cagatgtggt	180
gcgcatgctg	ctgtccctgc	agcccttctt	gca			213

<210> 85

<211> 273

<212> DNA

<213> mouse

<220>

<400> 85

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cactcccccg	tccatcctga	agcgggctcc	tcgggagcgt	ccaggtcacg	tgccctttaa	180
cggcatcacc	gtctactatt	tcccacgggtg	ccagggatcc	accagtgtgc	ccagccgtg	240
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<210> 86
 <211> 218
 <212> DNA
 <213> mouse

<400> 86

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cccagcctat	gtggagccta	tgactgtggt	ttgtcacc			218

<210> 87
 <211> 335
 <212> DNA
 <213> mouse

<400> 87

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ctgagctgtt	tcgtcctagt	tggtgagtta	agtggcatag	ccctcttgag	gcctctgatg	300
tggaaggggc	acagaattgc	aattattctt	gcatg			335

<210> 88
 <211> 410
 <212> DNA
 <213> mouse

<400> 88

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ttctgaaaac	aaaaccgtgt	caacttcttt	actttacaaa	tgcaagtttt	cagaatccac	360
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<210> 89
 <211> 279
 <212> DNA
 <213> mouse

<220>

<400> 89

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agaagagttt	atgggaaatc	ttggagaaaa	cattggatgg	tttgagagaa	tggttaggag	180
atcagactag	ctagtccagg	aagcagtga	ggggggcggg	gttagaagat	gaggtcagaa	240
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<210> 90
 <211> 398
 <212> DNA
 <213> mouse

<400> 90

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WO 99/55865

PCT/NZ99/00051

actcttagac	atgggtgtgc	tcactgaact	ctagggctctg	tgtgctagat	gctgccaacg	180
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ctgaagaaca	tctgttgcca	gaacggccac	accaaacaga	tggagtgcc	cagcacttag	300
cttcttaa	aacatcggaa	ccattcagcc	agcgagtctg	tgtttgctt	ttgttaaatt	360
gtccgcccga	tctaaattcc	tccaaaaggc	ttgtgacc			398

<210> 91
 <211> 279
 <212> DNA
 <213> mouse

<400> 91

gttgttactt	cagttgctct	cggcgggaat	tcttaaactg	catcctgagt	gagggagctt	60
tggcgagaaa	gcaagaccca	gtggtagaca	gattagcatt	actgtacagc	ttctttgggt	120
gttcgaggaa	gcccggctgg	accatagtgg	ccacggcggt	gaggtaggcg	tggacagggc	180
tgaccagtcc	aagttaagga	cgttcgggtc	catgttaacc	ctgccttgta	cgtccagcat	240
cgtaagaaaa	aacacttgag	aaccgaaga	ggagatgga			279

<210> 92
 <211> 401
 <212> DNA
 <213> mouse

<400> 92

aaaaagtttt	acaaaaacct	tttattgact	tttataaatt	agatagtatt	tcaaagttta	60
tgtagaatcg	tattctttga	aactgtactt	agcagagcag	aagaggcctg	ctgacgctag	120
cacgctctgc	aatgaatcat	gtggcaccga	gtctacgcca	aggccccga	gaaactttat	180
tccatagatg	ggcagatgg	tcccaaagt	acactacaga	actacaaatc	gactcttaaa	240
attaaaacgg	gactttacaa	gcattctaga	agactcaaac	ttgaagcaat	ttttggaaaa	300
taaatgtaca	gagaaaagat	cttgaagcta	ctgaacagag	aaccctcatt	aaccgagcaa	360
atacatccta	tggagcttcc	gaggagtaca	cagacagacc	g		401

<210> 93
 <211> 339
 <212> DNA
 <213> mouse

<400> 93

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ccagcagtgc	ctcggtaccc	agaagacggg	ctgtctcccc	ccaaaagacg	gcgacattcg	120
atgagaagtc	accacagtga	tctcacattt	tgcgagatta	tcctgatgga	gatggagtcc	180
catgatgcag	cctggccttt	cctagagcct	gtgaaccctc	gcttggtgag	tggataccga	240
cgtgtcatca	agaaccctat	ggatttttcc	accatgcgag	aacgcctgct	ccgtggaggg	300
tacactagct	cagaagagtt	tgcagctgat	gctctgctg			339

<210> 94
 <211> 55
 <212> DNA
 <213> mouse

<400> 94

gggggtgtggg	caacttggat	aacctcagct	gcttccatct	ggctgacatc	tttgg	55
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<210> 95
 <211> 186
 <212> DNA
 <213> mouse

<400> 95

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gcggggcccc	agaaacaaga	agcgcggtcg	gaggaggctc	gccgaggagc	cgctgggggt	120

agagggtcgac cagttcctgg aagacgtccg gctacaggag cgcacgaccg gtggcttgtt 180
ggcaga 186

<210> 96
<211> 244
<212> DNA
<213> mouse

<400> 96
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ccctctcccc aaggccatgg attatgaagc ccctctgtaa gatggtgagc caggggccct 120
aagagggcat gaggcacacc ctgatcactg tctcaggcct ttgtgggcac tgactcgacc 180
ctggcccacc tcacgcccc aggccagttg gcaactgggtg gctcttgagg gctcttacgc 240
cctt 244

<210> 97
<211> 116
<212> DNA
<213> mouse

<220>
<221> unsure
<222> (11) ... (11)

<221> unsure
<222> (13) ... (13)

<221> unsure
<222> (41) ... (41)

<400> 97
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atctaggact cctgccaccc tgactgctga cttacagcta tgagggtccc gcttct 116

<210> 98
<211> 307
<212> DNA
<213> mouse

<400> 98
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cgaattcatg acacctgtga tccaggacaa cccctcaggc tgggggtccct gtgccgttcc 120
tgagcaattt cgggatatgc cctaccagcc attcagcaaa ggagatcggc tgggaaaggt 180
tgcagactgg acaggggcca cataccagga caagaggtac acaaacaagt attcctctca 240
gttcgggtggg gggagtcagt atgcatattt ccatgaggag gatgagacaa gctttccagc 300
tgggtgg 307

<210> 99
<211> 360
<212> DNA
<213> mouse

<220>

<400> 99
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tgggaaccag acagccttgc ttcactgtat aagtgccctg atcacacgca gaatgaagtg 180
ccaggttgct cagaagcaca aagggtgtgg ctactggccc taaccatgga ctacgtggtt 240
ctaaccaaag actctagaac tctgggggtgg gggagaaaca atgtgttctg tgctccagaa 300

ctcggctt cctggcccat atggatgggc ttggcaagga acctacctt tctctaaggt 360

<210> 100
<211> 257
<212> DNA
<213> mouse

<400> 100
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tctccttaga cgccggcgac ccaggacgag ggcttcatca ctgtaaattg ttgcaagccg 180
acaaagctgc acctcctgaa aaagacggac agcccatcgc gtgagctgta gaaatttgtg 240
gacgcatttc tatcggt 257

<210> 101
<211> 203
<212> DNA
<213> mouse

<400> 101
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gcacccctcaa gagggcccacc agcaacgggtg tggtcagcag ccccaactcc accagcaggc 120
cagcccttcc tgtcaagtcc ctacgacagc gggaggcaga gtatgcagag gctcggagac 180
ggatcctagg cagtgccagc cct 203

<210> 102
<211> 300
<212> DNA
<213> mouse

<400> 102
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agccaacccc aactcagcca tctttggggg agccaggccc agagaggaag tggttcagaa 120
ggagcaagaa tgagcttagg ttgggaggga atggggcggtg ggggagctgg agcaagacca 180
cggcctgggtg gcagccggtc gccctacagg cccatttccc gcctggcact gtcctcctta 240
cagcggaaac acagagcttg tgagtgcatt tcagctgtta acaagtgggt tctagtacat 300

<210> 103
<211> 370
<212> DNA
<213> mouse

<220>

<400> 103
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gccatggaga tcctcaaagt gctctttaat atcacctttg actctgtcaa gagggaggtt 180
gatgaggaag atgctgccct ttaccgggtac ctgggggactc ttctgcggca ctgcgtgatg 240
gttgaagctg ctgggggaccg cacagaggag ttccacggcc acacgggtgaa tctcctgggg 300
aacttgcccc tcaagtgttt ggatgtgctt ctggccctgg agctccacga aggatcctta 360
gagtcaatgg 370

<210> 104
<211> 423
<212> DNA
<213> mouse

<400> 104
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tcctaccttg cctgtcttct ctctcctggg aagatgttcc tgggtggggct gacgggaggc	120
atcgccctcag gcaagagctc cgtcacccag gtattccaac agctgggctg tgctgtaatc	180
gacgtggacg tcattgcgcg gcacgttgtc cagccagggt atcctgcca cgggcgtata	240
gtagaggcct ttggcactga agtcttgctg gagaatggcg acatcgaccg caaggtcctc	300
ggagacctga tcttcaacca gcctgaccgt cggcagctgc tcaactccat taccaccct	360
gagatccgca aggaaatgat gaaggagacc ttcaagtact tctccgaggt accgatacgt	420
gat	423

<210> 105
 <211> 117
 <212> DNA
 <213> mouse

<400> 105	
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gcccgcgctcg gtgactgggg tctcacacag gttcagcact tggagcatag tgagggtg	117

<210> 106
 <211> 133
 <212> DNA
 <213> mouse

<400> 106	
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tccccttctc attcattcca gactttcaag tgttttcttc aatactgagg ctttctcctg	120
cagctctggg ctg	133

<210> 107
 <211> 217
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (1)...(1)

<221> unsure
 <222> (11)...(11)

<221> unsure
 <222> (18)...(23)

<221> unsure
 <222> (34)...(34)

<221> unsure
 <222> (37)...(38)

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 <222> (40)...(42)

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 <222> (50)...(52)

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 <222> (55)...(58)

<221> unsure
 <222> (152)...(152)

<221> unsure

<222> (155) ... (155)

<221> unsure

<222> (165) ... (165)

<400> 107

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ccaaagcagc	ggccgcggcc	ggagccctc	ancancccca	ccaangcggg	cactttcatc	180
gccccctctg	tctactccaa	catcacccct	taccaga			217

<210> 108

<211> 346

<212> DNA

<213> mouse

<220>

<400> 108

gggcatagaa	ggcatctcga	aaagaatact	tattttgaatt	gaaggaagat	gaagaggcct	60
gcaggaaggc	tcagaagaca	ggagtgtttt	acctctttca	tgacctggat	cctttgctcc	120
aggcgtcagg	acatcgatac	ctggtgcccc	ggcttagccg	agcagagttg	gaagggctgc	180
tgggtaagtt	cggacaggat	tcgcaaagaa	ttgaagattc	ggtgctggtt	gggtgctccg	240
agcagcagga	agcatggttt	gctttggatc	taggtctgaa	gagtgcctcc	tccagccgtg	300
gacaagtatc	gctgctccag	cagcttgact	gctgtaaaga	ggatct		346

<210> 109

<211> 242

<212> DNA

<213> mouse

<400> 109

ccacattgtc	cacaactgga	aggcacgatg	gttcatectt	cggcagaaca	cgctcctgta	60
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ctgcaccatc	acctgcccc	gcctggagta	tgaaaaccgg	ccgctcctca	ttaaactgaa	180
gacccgaact	tccactgagt	acttcctgga	agcctgttct	cgagaggaga	gagactcctg	240
gg						242

<210> 110

<211> 310

<212> DNA

<213> mouse

<220>

<400> 110

cccggccggg	aatccagggtg	gtagctgggtg	gagtcgcctc	cggagagtga	cgcgagact	60
cggtcccccc	gcggcccgc	ctcctgccc	cctcgccgcg	gtctcccttg	ctccctgaga	120
tcgctgagcg	ctgagcagcg	gcccgggaga	ggaggccttg	ggcgacgggg	cgcgagagg	180
gagggcgggc	gggcagtggg	ggcgccgcgg	atctctatat	ggcgacggct	ctgtcgggtc	240
tggtgtccg	gctgtcgcgc	tcggccgnc	cgcccgtcc	tatggggtct	tctgcaa-gg	300
ggctgaccgc						310

<210> 111

<211> 228

<212> DNA

<213> mouse

<400> 111

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gccctcaacc	ccccaaactcc	tttggtatga	agtactttta	acatttatat	ttcattgtta	120

cacttttaaatt tttgtaagga aaactctgat atttcattcc tcctgaacca ctaatggttag 180
 aattttatttc taagaatcag tcaacatgta tactcttaat agtgaatt 228

<210> 112
 <211> 292
 <212> DNA
 <213> mouse

<400> 112
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 ctgggtggcat ggactatggg atgggtgggt gcaaggaggc tgggaccgag tctcgcttca 120
 aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc 180
 acaaaaacgg cgctatagtg gccctgggta agacccgagg aggttcacca tacaaccagt 240
 ttgatataat cccagggtgac acactggggtg gccatacggg tcctgctggg ga 292

<210> 113
 <211> 255
 <212> DNA
 <213> mouse

<220>

<400> 113
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 caaccagaaa aagacctcag caatgtatag acctggaata tatagtgttg ccttgggtta 120
 actacaagaa cagccacgtg atcacagttt gaggggtggaa ggcaggggtg tgactgagtt 180
 ttgttttaacg gcctaaccga aaagcaaaga atcaaccatt tcttctactt gtggcaagaa 240
 acgagagtca tgggtg 255

<210> 114
 <211> 197
 <212> DNA
 <213> mouse

<400> 114
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 tgcattgtgc ctcttgggtc ttccacttat tgccctcgttc gtaagaaacc aaccataagg 120
 tgccaaggag gttttattcc tttttttttt aaagatgaca aatgtacaga tgtagtaga 180
 gatgttaatg tacagat 197

<210> 115
 <211> 205
 <212> DNA
 <213> mouse

<400> 115
 aaaacatttc acaaaacagc aaaacaaaat tgatacaatc aaaaaaacia cactataacc 60
 aacataggtg aaaacagcca aacacataat gtacaatctg gtgttccagg acaaacatct 120
 gtcataatca tggatatata atatatactt tttcactcaa tatattatga caatatatat 180
 ttaaaatttt gttatagaca aaaaa 205

<210> 116
 <211> 202
 <212> DNA
 <213> mouse

<220>

<400> 116
 cctccctcat cctctacttc ccttttcttc cctgcttgat tttctcattc cagaccctta 60

tgcacacaca	cacacacaca	cacacacaca	cacgaacaca	cgcacacaca	cacacacacg	120
cacacacaca	ctgtccatcc	atagttactt	atttagtttt	ccattcctag	agagatctaa	180
tcacccccta	gtcagtgcct	aa				202

<210> 117
 <211> 240
 <212> DNA
 <213> mouse

<400> 117						
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cgcttctgct	gtgtgaagga	gcgcaagccc	tggagtgcct	cagctgcgtg	cagaaggcgg	120
acgatggatg	cgtccgcac	aggatgaaga	cagtcaaatg	tgggtcccggg	gtggacgtct	180
gtaccgaggg	cgtgggagcg	gtagagacca	tccacgggca	attctctgtg	gcggtgcggg	240

<210> 118
 <211> 527
 <212> DNA
 <213> Human

<400> 118						
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gtgactgtaa	cacctccaat	cacagcccag	caaggtaact	ggacagttaa	caaaacagaa	180
gtcacaaca	tagaaggacc	catagccttg	aagttctcac	acctttgcct	ggaagatcat	240
aacagttact	gcatacaacg	tgcttgtgca	ttccaccatg	agctagagaa	agccatctgc	300
aggtgtttta	ctgggtatac	tggagaaagg	tgtgagcact	tgactttaac	ttcatatgct	360
gtggattctt	atgaaaaata	cattgcaatt	gggattgggt	ttggattact	attaagtggg	420
tttcttggtt	ttttttactg	ctatataaga	aagaggtgtc	taaaattgaa	atcgccctac	480
aatgtctggt	ctggagaaag	acgaccactg	tgaggccttt	gtgaaga		527

<210> 119
 <211> 655
 <212> DNA
 <213> Rat

<400> 119						
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cccccagtac	ggctcttcac	cgaggaggag	ctggcccgcct	acagcggcga	ggaggaggat	180
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tatggacgtg	gagcccccta	caacgccttg	gccgggaagg	actcgagcag	aggtgtggcc	300
aagatgtcgc	tggatcctgc	agacctcact	catgacattt	ctgggtctcac	tgccaaggag	360
ctggaagccc	tcgatgacat	cttcagcaag	gtgtacaaag	ccaaataccc	cattgttggc	420
tacacggccc	gcaggatcct	caacgaggat	ggcagcccca	acctggactt	caagcctgaa	480
gaccagcccc	atthttgacat	aaaggacgag	ttctaattgtc	tagctgagaa	gctgggttcta	540
gggagaggtg	aggggacagg	agttaaatgt	cccacgggaac	aagcagggga	agcctctgag	600
tgctctgcat	ctgaataaaa	ctgatattta	actgggaaaa	aaaaaaaaaa	aaaaa	655

<210> 120
 <211> 176
 <212> PRT
 <213> Rat

<400> 120														
Met	Val	Pro	Cys	Phe	Leu	Leu	Ser	Leu	Leu	Leu	Val	Arg	Pro	Ala
1			5					10					15	
Pro	Val	Val	Ala	Tyr	Ser	Val	Ser	Leu	Pro	Ala	Ser	Phe	Leu	Glu
			20					25					30	
Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser	Ala	Ser	Ser	Pro
		35					40					45		

Leu Leu Pro Pro Arg Thr Pro Ala Phe Ser Pro Thr Pro Gly Arg Thr
 50 55 60
 Gln Pro Thr Ala Pro Val Gly Pro Val Pro Pro Thr Asn Leu Leu Asp
 65 70 75 80
 Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val
 85 90 95
 Gly Ser Leu Thr Phe Leu Ile Met Phe Ile Val Cys Ala Ala Leu Ile
 100 105 110
 Thr Arg Gln Lys His Lys Ala Thr Ala Tyr Tyr Pro Ser Ser Phe Pro
 115 120 125
 Glu Lys Lys Tyr Val Asp Gln Arg Asp Arg Ala Gly Gly Pro His Ala
 130 135 140
 Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Gln Glu Glu Gly
 145 150 155 160
 Leu Asp Phe Phe Gln Gln Leu Gln Ala Asp Ile Leu Ala Cys Tyr Ser
 165 170 175

<210> 121
 <211> 116
 <212> PRT
 <213> Rat

<400> 121
 Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1 5 10 15
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
 20 25 30
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
 35 40 45
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
 50 55 60
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
 65 70 75 80
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
 85 90 95
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
 100 105 110
 Gln Lys Gln Gln
 115

<210> 122
 <211> 64
 <212> PRT
 <213> Human

<400> 122
 Met Asn Leu Leu Ile Gly Ser Ile Ile Leu Ser Ser Phe Leu Val Leu
 1 5 10 15
 Ser Asp Gly Asp Thr Thr Ala Ser Pro Ser Ser Met Ser Ser Ser
 20 25 30
 Val Leu Asn His Ile Ser Ser Ser Ser Ser Val Trp His Leu Phe
 35 40 45
 Asp Ile Cys Asp Ser Ser Lys Trp Asn Ala Tyr Cys Gln Val Trp Gly
 50 55 60

<210> 123
 <211> 68
 <212> PRT
 <213> Human

<400> 123

Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg
 1 5 10 15
 Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly
 20 25 30
 Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr
 35 40 45
 Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe
 50 55 60
 Ser Cys Leu Leu
 65

<210> 124
 <211> 110
 <212> PRT
 <213> mouse

<400> 124
 Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
 1 5 10 15
 Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
 20 25 30
 Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
 35 40 45
 Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
 50 55 60
 Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
 65 70 75 80
 Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
 85 90 95
 Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His
 100 105 110

<210> 125
 <211> 330
 <212> PRT
 <213> mouse

<400> 125
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 1 5 10 15
 Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
 20 25 30
 Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 35 40 45
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 50 55 60
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 65 70 75 80
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 85 90 95
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 100 105 110
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 115 120 125
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 130 135 140
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
 145 150 155 160
 Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 165 170 175
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp

		180						185					190				
Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Met	Cys	Ile	Glu	Ala	Ser	Tyr		
		195						200					205				
Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Lys	Cys	Pro	Phe	Gln	Ser	Trp		
		210						215					220				
Pro	Glu	Ala	Tyr	Gly	Ser	Asp	Phe	Trp	Gln	Ser	Ile	Arg	Phe	Thr	Asp		
225						230					235				240		
Tyr	Ser	Gln	His	Asn	Gln	Met	Val	Met	Ala	Leu	Thr	Leu	Arg	Cys	Pro		
				245					250					255			
Leu	Lys	Leu	Glu	Ala	Ser	Leu	Cys	Trp	Arg	Gln	Asp	Pro	Leu	Thr	Pro		
			260					265					270				
Cys	Glu	Thr	Leu	Pro	Asn	Ala	Thr	Ala	Gln	Glu	Ser	Glu	Gly	Trp	Tyr		
		275					280						285				
Ile	Leu	Glu	Asn	Val	Asp	Leu	His	Pro	Gln	Leu	Cys	Phe	Lys	Phe	Ser		
		290				295					300						
Phe	Glu	Asn	Ser	Ser	His	Val	Glu	Cys	Pro	His	Gln	Ser	Gly	Ser	Leu		
305					310					315					320		
Pro	Ser	Trp	Thr	Val	Ser	Met	Asp	Thr	Gln								
				325					330								

<210> 126

<211> 37

<212> PRT

<213> Rat

<400> 126

Met	Leu	Trp	Val	Leu	Leu	Ser	Leu	Thr	Pro	Leu	Leu	Ser	Pro	Leu	Ile		
1				5					10					15			
Phe	Phe	Pro	Val	Lys	Thr	Val	Ala	Leu	Glu	Glu	Ile	Ser	Thr	Ile	Cys		
			20					25					30				
Arg	Ala	Asp	Val	Leu													
			35														

<210> 127

<211> 42

<212> PRT

<213> mouse

<400> 127

Met	Gly	Ser	Pro	Ile	Ser	Gly	Val	Cys	Pro	Val	Leu	Pro	Gly	Gly	Leu		
1				5				10						15			
Phe	Val	Ala	Leu	Gly	Trp	Ile	Phe	Leu	Leu	Phe	His	Arg	Asp	Ala	Phe		
			20					25					30				
Ser	Leu	His	Thr	Met	Ser	Ala	Gly	Phe	Pro								
			35				40										

<210> 128

<211> 253

<212> PRT

<213> mouse

<400> 128

Met	Met	Tyr	Trp	Ile	Val	Phe	Ala	Ile	Phe	Met	Ala	Ala	Glu	Thr	Phe		
1				5					10					15			
Thr	Asp	Ile	Phe	Ile	Ser	Trp	Ser	Gly	Pro	Arg	Ile	Gly	Arg	Pro	Trp		
			20					25					30				
Gly	Trp	Glu	Gly	Pro	His	His	His	His	His	Leu	Ala	Ser	Gly	Ser	His		
			35				40					45					
Lys	Pro	Leu	Pro	Leu	Leu	Thr	His	Arg	Phe	Pro	Phe	Tyr	Tyr	Glu	Phe		
			50			55					60						
Lys	Met	Ala	Phe	Val	Leu	Trp	Leu	Leu	Ser	Pro	Tyr	Thr	Lys	Gly	Ala		

65					70					75					80
Ser	Leu	Leu	Tyr	Arg	Lys	Phe	Val	His	Pro	Ser	Leu	Ser	Arg	His	Glu
				85					90					95	
Lys	Glu	Ile	Asp	Ala	Cys	Ile	Val	Gln	Ala	Lys	Glu	Arg	Ser	Tyr	Glu
			100					105					110		
Thr	Met	Leu	Ser	Phe	Gly	Lys	Arg	Ser	Leu	Asn	Ile	Ala	Ala	Ser	Ala
		115					120					125			
Ala	Val	Gln	Ala	Ala	Thr	Lys	Ser	Gln	Gly	Ala	Leu	Ala	Gly	Arg	Leu
	130					135					140				
Arg	Ser	Phe	Ser	Met	Gln	Asp	Leu	Arg	Ser	Ile	Pro	Asp	Thr	Pro	Val
145					150				155						160
Pro	Thr	Tyr	Gln	Asp	Pro	Leu	Tyr	Leu	Glu	Asp	Gln	Val	Pro	Arg	Arg
			165					170					175		
Arg	Pro	Pro	Ile	Gly	Tyr	Arg	Pro	Gly	Gly	Leu	Gln	Gly	Ser	Asp	Thr
		180					185					190			
Glu	Asp	Glu	Cys	Trp	Ser	Asp	Asn	Glu	Ile	Val	Pro	Gln	Pro	Pro	Val
	195					200					205				
Arg	Pro	Arg	Glu	Lys	Pro	Leu	Gly	Arg	Ser	Gln	Ser	Leu	Arg	Val	Val
	210				215					220					
Lys	Arg	Lys	Pro	Leu	Thr	Arg	Glu	Gly	Thr	Ser	Arg	Ser	Leu	Lys	Val
225				230					235						240
Arg	Thr	Arg	Lys	Lys	Ala	Met	Pro	Ser	Asp	Met	Asp	Ser			
			245						250						

<210> 129
 <211> 40
 <212> PRT
 <213> mouse

<400> 129
 Met Lys Ala Met Ala Leu Ser Leu Gly Ala Ser Pro Val Leu Ala Phe
 1 5 10 15
 Leu Leu Ser Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly
 20 25 30
 Ser Lys Val Pro Gln Phe Leu Asn
 35 40

<210> 130
 <211> 87
 <212> PRT
 <213> mouse

<400> 130
 Met Ile Ala Val Thr Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg
 1 5 10 15
 Ile Ser Thr Ala Ala Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg
 20 25 30
 Ser Asn Ile Arg Val Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu
 35 40 45
 Val Val Ile Ile Leu Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp
 50 55 60
 Leu Thr Lys Ile Gly Glu Cys His Val Gln Asp Ser Ile Gly Ser Met
 65 70 75 80
 Gly Leu Gly Gln Gly Gln Pro
 85

<210> 131
 <211> 70
 <212> PRT
 <213> mouse

<400> 131

Met Phe Gly Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys
 1 5 10 15
 Val Cys Val Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro
 20 25 30
 Cys Gly Cys Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu
 35 40 45
 Ser Leu His Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro
 50 55 60
 Gly Leu Ser Leu Ile Ser
 65 70

<210> 132

<211> 63

<212> PRT

<213> mouse

<400> 132

Met Trp Leu Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala
 1 5 10 15
 Phe Val Thr Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met
 20 25 30
 Ser Leu His Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly
 35 40 45
 Val Pro Leu Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu
 50 55 60

<210> 133

<211> 39

<212> PRT

<213> mouse

<400> 133

Met Asp Asn Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala
 1 5 10 15
 Ile Ser Val Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe
 20 25 30
 Ser Lys Asp Leu Glu Val Thr
 35

<210> 134

<211> 90

<212> PRT

<213> Rat

<400> 134

Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
 1 5 10 15
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
 20 25 30
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
 35 40 45
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
 50 55 60
 Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe
 65 70 75 80
 Ala Gly Glu Val Leu Gly Ile Cys His Ser
 85 90

<210> 135

<211> 193

<212> PRT

<213> Rat

<400> 135

Met	Thr	Ser	Gly	Pro	Gly	Gly	Pro	Ala	Ala	Ala	Thr	Gly	Gly	Gly	Lys
1				5					10					15	
Asp	Thr	His	Gln	Trp	Tyr	Val	Cys	Asn	Arg	Glu	Lys	Leu	Cys	Glu	Ser
			20					25					30		
Leu	Gln	Ser	Val	Phe	Val	Gln	Ser	Tyr	Leu	Asp	Gln	Gly	Thr	Gln	Ile
		35					40					45			
Phe	Leu	Asn	Asn	Ser	Ile	Glu	Lys	Ser	Gly	Trp	Leu	Phe	Ile	Gln	Leu
	50					55					60				
Tyr	His	Ser	Phe	Val	Ser	Ser	Val	Phe	Thr	Leu	Phe	Met	Ser	Arg	Thr
65					70					75				80	
Ser	Ile	Asn	Gly	Leu	Leu	Gly	Arg	Gly	Ser	Met	Phe	Val	Phe	Ser	Pro
			85					90						95	
Asp	Gln	Phe	Gln	Arg	Leu	Leu	Lys	Ile	Asn	Pro	Asp	Trp	Lys	Thr	His
			100					105					110		
Arg	Leu	Leu	Asp	Leu	Gly	Ala	Gly	Asp	Gly	Glu	Val	Thr	Lys	Ile	Met
		115					120					125			
Ser	Pro	His	Phe	Glu	Glu	Ile	Tyr	Ala	Thr	Glu	Leu	Ser	Glu	Thr	Met
	130					135					140				
Ile	Trp	Gln	Leu	Gln	Lys	Lys	Lys	Tyr	Arg	Val	Leu	Gly	Ile	Asn	Glu
145					150					155					160
Trp	Gln	Asn	Thr	Gly	Phe	Gln	Tyr	Asp	Val	Ile	Ser	Cys	Leu	Asn	Leu
				165					170					175	
Leu	Asp	Arg	Cys	Asp	Gln	Pro	Leu	Thr	Leu	Leu	Lys	Asp	Ile	Arg	Met
			180					185					190		
Ser															

<210> 136

<211> 106

<212> PRT

<213> Rat

<400> 136

Met	Ala	Ala	Pro	Met	Asp	Arg	Thr	His	Gly	Gly	Arg	Ala	Ala	Arg	Ala
1				5					10					15	
Leu	Arg	Arg	Ala	Leu	Ala	Leu	Ala	Ser	Leu	Ala	Gly	Leu	Leu	Leu	Ser
			20					25					30		
Gly	Leu	Ala	Gly	Ala	Leu	Pro	Thr	Leu	Gly	Pro	Gly	Trp	Arg	Arg	Gln
		35					40					45			
Asn	Pro	Glu	Pro	Pro	Ala	Ser	Arg	Thr	Arg	Ser	Leu	Leu	Leu	Asp	Ala
	50					55					60				
Ala	Ser	Gly	Gln	Leu	Arg	Leu	Glu	Tyr	Gly	Phe	His	Pro	Asp	Ala	Val
65					70					75					80
Ala	Trp	Ala	Asn	Leu	Thr	Asn	Ala	Ile	Arg	Glu	Thr	Gly	Trp	Ala	Tyr
			85						90					95	
Leu	Asp	Leu	Gly	Thr	Asn	Gly	Ser	Tyr	Lys						
			100					105							

<210> 137

<211> 286

<212> PRT

<213> Rat

<400> 137

Met	Ala	Ala	Ala	Met	Pro	Leu	Gly	Leu	Ser	Leu	Leu	Leu	Leu	Val	Leu
1				5					10					15	
Val	Gly	Gln	Gly	Cys	Cys	Gly	Arg	Val	Glu	Gly	Pro	Arg	Asp	Ser	Leu

<210>	138
<211>	198
<212>	PRT
<213>	Rat

	<400> 138														
Met 1	Thr	Val	Phe	Arg	Lys	Val	Thr	Thr	Met	Ile	Ser	Trp	Met	Leu	Leu
				5					10					15	
Ala	Cys	Ala	Leu	Pro	Cys	Ala	Ala	Asp	Pro	Met	Leu	Gly	Ala	Phe	Ala
			20					25					30		
Arg	Arg	Asp	Phe	Gln	Lys	Gly	Gly	Pro	Gln	Leu	Val	Cys	Ser	Leu	Pro
		35					40					45			
Gly	Pro	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Pro	Gly	Ser	Ser	Gly
	50					55					60				
Met 65	Val	Gly	Arg	Met	Gly	Phe	Pro	Gly	Lys	Asp	Gly	Gln	Asp	Gly	Gln
					70					75					80
Asp	Gly	Asp	Arg	Gly	Asp	Ser	Gly	Glu	Glu	Gly	Pro	Pro	Gly	Arg	Thr
				85					90					95	
Gly	Asn	Arg	Gly	Lys	Gln	Gly	Pro	Lys	Gly	Lys	Ala	Gly	Ala	Ile	Gly
			100					105					110		
Arg	Ala	Gly	Pro	Arg	Gly	Pro	Lys	Gly	Val	Ser	Gly	Thr	Pro	Gly	Lys
		115					120					125			
His	Gly	Ile	Pro	Gly	Lys	Lys	Gly	Pro	Lys	Gly	Lys	Lys	Gly	Glu	Pro
	130					135					140				
Gly 145	Leu	Pro	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Ser	Arg	Ala	Lys	Ser	Ala
					150					155					160
Phe	Ser	Val	Ala	Val	Thr	Lys	Ser	Tyr	Pro	Arg	Glu	Arg	Leu	Pro	Ile

165
 Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
 180
 Ser Gly Lys Phe Val Cys
 195

<210> 139
 <211> 233
 <212> PRT
 <213> Rat

<400> 139
 Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1 5 10 15
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20 25 30
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35 40 45
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50 55 60
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65 70 75 80
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85 90 95
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
 100 105 110
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
 115 120 125
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
 130 135 140
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
 145 150 155 160
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
 165 170 175
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
 180 185 190
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys
 195 200 205
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
 210 215 220
 Glu Asp Thr Glu Phe Leu Gln Pro Gly
 225 230

<210> 140
 <211> 38
 <212> PRT
 <213> Human

<400> 140
 Met Gly Leu Ala Leu Cys Leu Ala Ser Ala Gly Ile Ser Gly Ser Arg
 1 5 10 15
 Ser Ala Phe Leu Gly Val Pro Arg Pro Arg Pro Thr Leu Ile Lys Leu
 20 25 30
 Ile Asp Thr Val Asp Leu
 35

<210> 141
 <211> 322
 <212> PRT
 <213> mouse

<400> 141
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
 20 25 30
 Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
 85 90 95
 Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
 100 105 110
 Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
 115 120 125
 Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
 275 280 285
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
 290 295 300
 Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
 305 310 315 320
 Gln Gly

<210> 142
 <211> 312
 <212> PRT
 <213> mouse

<400> 142
 Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
 1 5 10 15
 Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
 20 25 30
 Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
 35 40 45
 Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
 50 55 60
 Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
 65 70 75 80
 Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly

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<210> 143
<211> 163
<212> PRT
<213> Rat
```

<210> 144
<211> 330

<212> PRT

<213> Rat

<400> 144

Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1 5 10 15
 Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
 20 25 30
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35 40 45
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50 55 60
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65 70 75 80
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85 90 95
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
 100 105 110
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
 115 120 125
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
 130 135 140
 Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
 145 150 155 160
 Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
 165 170 175
 Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
 180 185 190
 Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
 195 200 205
 Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
 210 215 220
 Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
 225 230 235 240
 Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
 245 250 255
 Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
 260 265 270
 Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
 275 280 285
 Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
 290 295 300
 Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
 305 310 315 320
 His Arg Lys Ala Phe Leu Pro Phe Leu Phe
 325 330

<210> 145

<211> 301

<212> PRT

<213> Rat

<400> 145

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1 5 10 15
 Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
 20 25 30
 Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
 35 40 45
 Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
 50 55 60

Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
 65 70 75 80
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
 85 90 95
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
 100 105 110
 Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
 115 120 125
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
 130 135 140
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
 145 150 155 160
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
 165 170 175
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
 180 185 190
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
 195 200 205
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
 210 215 220
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
 225 230 235 240
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
 245 250 255
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
 260 265 270
 Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
 275 280 285
 Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
 290 295 300

<210> 146
 <211> 61
 <212> PRT
 <213> Rat

<400> 146

Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
 1 5 10 15
 His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
 20 25 30
 Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
 35 40 45
 Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
 50 55 60

<210> 147
 <211> 105
 <212> PRT
 <213> Rat

<400> 147

Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
 1 5 10 15
 Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
 20 25 30
 Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
 35 40 45
 Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile
 50 55 60
 Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu

65					70					75				80
Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg
				85					90					95
Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly						
			100					105						

<210> 148
 <211> 210
 <212> PRT
 <213> Rat

<400> 148

Met	Leu	Gly	Ala	Thr	Ser	Leu	Ser	Trp	Pro	Trp	Val	Leu	Trp	Ala	Val
1				5					10					15	
Ala	Gln	Arg	Asp	Ser	Val	Asp	Ala	Ile	Gly	Met	Phe	Leu	Gly	Gly	Leu
			20					25					30		
Val	Ala	Thr	Ile	Phe	Leu	Asp	Ile	Ile	Tyr	Ile	Ser	Ile	Phe	Tyr	Ser
		35					40					45			
Ser	Val	Ala	Val	Gly	Asp	Thr	Gly	Arg	Phe	Ser	Ala	Gly	Met	Ala	Ile
	50					55					60				
Phe	Ser	Leu	Leu	Leu	Gln	Ala	Leu	Leu	Leu	Leu	Pro	Arg	Leu	Pro	His
65					70					75				80	
Ala	Pro	Gly	Ser	Glu	Gly	Val	Ser	Ser	Arg	Ser	Ala	Arg	Ile	Ser	Ser
				85					90					95	
Asp	Leu	Leu	Arg	Asn	Ile	Val	Pro	Thr	Arg	Gln	Leu	Thr	Arg	Gln	Thr
			100					105					110		
His	Leu	Gln	Thr	Pro	Leu	Gln	Ala	Trp	Arg	Thr	Arg	Ala	Lys	Leu	Pro
		115					120					125			
Pro	Gly	Gly	Thr	Glu	Ala	Val	Pro	Gly	Arg	Pro	Gly	Ala	Gln	Gln	Asp
	130					135					140				
Ala	Cys	His	Leu	Leu	Tyr	Trp	Thr	Tyr	Asn	Gly	Val	Ser	Ser	Ile	Pro
145					150					155				160	
Cys	His	Arg	Gly	Gly	Leu	Ser	His	Val	Pro	Ser	Glu	Val	Pro	Ala	Glu
			165						170					175	
Lys	Ser	Pro	Val	Leu	Ile	Leu	His	Ala	Ala	Pro	Pro	Phe	Lys	Thr	Pro
			180					185					190		
Val	Asn	Pro	Trp	Ala	Arg	Thr	Val	Val	Gly	Phe	Phe	Pro	Ser	Ser	Pro
		195					200						205		
Ser	Leu														
	210														

<210> 149
 <211> 301
 <212> PRT
 <213> Rat

<400> 149

Met	Leu	Val	Ala	Phe	Leu	Gly	Ala	Ser	Ala	Val	Thr	Ala	Ser	Thr	Gly
1				5					10					15	
Leu	Leu	Trp	Lys	Lys	Ala	His	Ala	Glu	Ser	Pro	Pro	Ser	Val	Asn	Ser
			20					25					30		
Lys	Lys	Thr	Asp	Ala	Gly	Asp	Lys	Gly	Lys	Ser	Lys	Asp	Thr	Arg	Glu
		35					40					45			
Val	Ser	Ser	His	Glu	Gly	Ser	Ala	Ala	Asp	Thr	Ala	Ala	Glu	Pro	Tyr
	50					55					60				
Pro	Glu	Glu	Lys	Lys	Lys	Lys	Arg	Ser	Gly	Phe	Arg	Asp	Arg	Lys	Val
65					70					75				80	
Met	Glu	Tyr	Glu	Asn	Arg	Ile	Arg	Ala	Tyr	Ser	Thr	Pro	Asp	Lys	Ile
			85						90					95	
Phe	Arg	Tyr	Phe	Ala	Thr	Leu	Lys	Val	Ile	Asn	Glu	Pro	Gly	Glu	Thr
			100					105					110		

Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
 115 120 125
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
 130 135 140
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
 145 150 155 160
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
 165 170 175
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
 180 185 190
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
 195 200 205
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
 210 215 220
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
 225 230 235 240
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
 245 250 255
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
 260 265 270
 Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
 275 280 285
 Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
 290 295 300

<210> 150
 <211> 80
 <212> PRT
 <213> Human

<400> 150
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
 1 5 10 15
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
 20 25 30
 Phe Gln Asp Thr Lys Val Tyr Cys Thr Arg Glu Ser Asn Pro His Cys
 35 40 45
 Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala Phe Cys Lys Ala
 50 55 60
 Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys His Pro Gly Lys Cys
 65 70 75 80

<210> 151
 <211> 27
 <212> PRT
 <213> mouse

<400> 151
 Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
 1 5 10 15
 Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
 20 25

<210> 152
 <211> 86
 <212> PRT
 <213> mouse

<400> 152
 Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
 1 5 10 15

Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
 20 25 30
 Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
 35 40 45
 Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly
 50 55 60
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
 65 70 75 80
 Leu Leu Ser Phe Pro Pro
 85

<210> 153
 <211> 72
 <212> PRT
 <213> mouse

<400> 153
 Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu
 1 5 10 15
 Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu
 20 25 30
 Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg
 35 40 45
 Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met
 50 55 60
 Ala Phe Ser Ile Leu Phe Ile Gln
 65 70

<210> 154
 <211> 169
 <212> PRT
 <213> mouse

<400> 154
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20 25 30
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35 40 45
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50 55 60
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65 70 75 80
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85 90 95
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
 100 105 110
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
 115 120 125
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
 130 135 140
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
 145 150 155 160
 Gly Glu Met Pro Pro Glu Asp Gly Met
 165

<210> 155
 <211> 61
 <212> PRT
 <213> mouse

<400> 155

Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
 1 5 10 15
 Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
 20 25 30
 Thr Val Thr Gln Met Arg Thr Ile Ile Thr Met Asp Gln Leu Arg
 35 40 45
 Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
 50 55 60

<210> 156

<211> 131

<212> PRT

<213> mouse

<400> 156

Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
 1 5 10 15
 Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
 20 25 30
 Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
 35 40 45
 Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
 50 55 60
 Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
 65 70 75 80
 Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
 85 90 95
 Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
 100 105 110
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
 115 120 125
 Leu Arg Arg
 130

<210> 157

<211> 133

<212> PRT

<213> mouse

<400> 157

Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
 20 25 30
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 35 40 45
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Glu His Val
 50 55 60
 Gln Gly Thr Gly Ala Arg Ser Thr Ala Cys Thr Leu Ser Cys Arg Ala
 65 70 75 80
 Pro Asn Ala Ser Ser Ser Gly Thr Met Pro Gly Thr Arg Ser Ala Gly
 85 90 95
 Ser Thr Lys Asn Arg Val Asp Asp His Gly Lys Lys Asn Ser Arg Pro
 100 105 110
 Val Glu Arg Leu Gln Gln Arg Thr Leu Gln Ile Lys Ile Lys Ala Leu
 115 120 125
 Ser Phe Ser Gln Ala
 130

<210> 158
 <211> 78
 <212> PRT
 <213> mouse

<400> 158
 Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
 1 5 10 15
 Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
 20 25 30
 Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
 35 40 45
 Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
 50 55 60
 Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
 65 70 75

<210> 159
 <211> 206
 <212> PRT
 <213> mouse

<400> 159
 Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
 1 5 10 15
 Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
 20 25 30
 Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
 35 40 45
 Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
 50 55 60
 Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
 65 70 75 80
 Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
 85 90 95
 Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
 100 105 110
 Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser
 115 120 125
 Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
 130 135 140
 Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
 145 150 155 160
 Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
 165 170 175
 His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
 180 185 190
 Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser
 195 200 205

<210> 160
 <211> 169
 <212> PRT
 <213> mouse

<400> 160
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20 25 30
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly

35	40	45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln		
50	55	60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu		
65	70	75
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr		80
85	90	95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly		
100	105	110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe		
115	120	125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu		
130	135	140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu		
145	150	155
Gly Glu Met Pro Pro Glu Asp Gly Met		160
165		

<210> 161
 <211> 114
 <212> PRT
 <213> mouse

<400> 161
Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
1 5 10 15
Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
20 25 30
Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
35 40 45
Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
50 55 60
His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
65 70 75 80
Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
85 90 95
Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
100 105 110
Ser Leu

<210> 162
 <211> 46
 <212> PRT
 <213> mouse

<400> 162
Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
1 5 10 15
Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
20 25 30
Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
35 40 45

<210> 163
 <211> 122
 <212> PRT
 <213> mouse

<400> 163
Met Phe Thr Phe Val Val Leu Val Ile Thr Ile Val Ile Cys Leu Cys

1 5 10 15
 His Val Cys Phe Gly His Phe Lys Tyr Leu Ser Ala His Asn Tyr Lys
 20 25 30
 Ile Glu His Thr Glu Thr Asp Ala Val Ser Ser Arg Ser Asn Gly Arg
 35 40 45
 Pro Pro Thr Ala Gly Ala Val Pro Lys Ser Ala Lys Tyr Ile Ala Gln
 50 55 60
 Val Leu Gln Asp Ser Glu Gly Asp Gly Asp Gly Ala Pro Gly
 65 70 75 80
 Ser Ser Gly Asp Glu Pro Pro Ser Ser Ser Gln Asp Glu Glu Leu
 85 90 95
 Leu Met Pro Pro Asp Gly Leu Thr Asp Thr Asp Phe Gln Ser Cys Glu
 100 105 110
 Asp Ser Leu Ile Glu Asn Glu Ile His Gln
 115 120

<210> 164

<211> 60

<212> PRT

<213> Rat

<400> 164

Met Ser Phe Val Lys Ile Glu Ala Thr Pro Thr Gln Thr Lys Trp Pro
 1 5 10 15
 Phe Ser Val Val Pro Gln Ser Leu Leu Val Thr Val Tyr Ile Cys Tyr
 20 25 30
 Ile Phe Leu Val Ile Phe Phe Phe Phe Glu Ala Cys Gln Glu Val
 35 40 45
 Leu Cys Ser Phe Phe Asp Phe Ser Arg Arg Arg Gly
 50 55 60

<210> 165

<211> 57

<212> PRT

<213> mouse

<400> 165

Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
 1 5 10 15
 Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
 20 25 30
 Ser Leu His Thr Met Ser Ala Gly Phe Pro Lys Ser Pro Ala Asn Pro
 35 40 45
 His His Pro Pro Leu Arg Leu Ser Pro
 50 55

<210> 166

<211> 75

<212> PRT

<213> mouse

<400> 166

Lys Thr Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp
 1 5 10 15
 Phe Met Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro
 20 25 30
 Phe Pro Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys
 35 40 45
 Gln Trp Glu Gly Ser Thr Met Thr His Thr His Thr His Thr His Ile
 50 55 60
 His Ile His Thr Pro Pro Arg Gln Cys Gln Ser

65

70

75

<210> 167
 <211> 52
 <212> PRT
 <213> mouse

<400> 167

Val	Arg	Ser	Leu	Glu	Gln	Leu	Gly	Leu	Phe	Ser	Val	Asp	Phe	Met	Val
1				5					10					15	
Cys	Ile	Phe	Leu	Phe	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Pro	Phe	Pro	Leu
			20					25					30		
Phe	Leu	Val	Arg	Lys	His	Ile	Leu	Leu	Ser	His	Cys	Lys	Gln	Trp	Glu
			35				40					45			
Gly	Ser	Thr	Met												
			50												

<210> 168
 <211> 119
 <212> PRT
 <213> Rat

<400> 168

Met	Leu	Gly	Ala	Thr	Ser	Leu	Ser	Trp	Pro	Trp	Val	Leu	Trp	Ala	Val
1				5					10					15	
Ala	Gln	Arg	Asp	Ser	Val	Asp	Ala	Ile	Gly	Met	Phe	Leu	Gly	Gly	Leu
			20					25					30		
Val	Ala	Thr	Ile	Phe	Leu	Asp	Ile	Ile	Tyr	Ile	Ser	Ile	Phe	Tyr	Ser
			35				40					45			
Ser	Val	Ala	Val	Gly	Asp	Thr	Gly	Arg	Phe	Ser	Ala	Gly	Met	Ala	Ile
			50			55					60				
Phe	Ser	Leu	Leu	Leu	Gln	Ala	Leu	Leu	Leu	Leu	Pro	Arg	Leu	Pro	His
65					70					75					80
Ala	Pro	Gly	Ser	Glu	Gly	Val	Ser	Ser	Arg	Ser	Ala	Arg	Ile	Ser	Ser
				85					90					95	
Asp	Leu	Leu	Arg	Asn	Ile	Val	Pro	Thr	Arg	Gln	Leu	Thr	Arg	Gln	Thr
			100					105						110	
His	Leu	Gln	Thr	Pro	Leu	Gln									
			115												

<210> 169
 <211> 104
 <212> PRT
 <213> Rat

<220>

<400> 169

Leu	Val	Pro	Lys	Ser	Ala	Arg	Ala	Ser	Leu	Leu	Cys	Cys	Gly	Pro	Lys
1				5					10					15	
Leu	Ala	Ala	Cys	Gly	Ile	Val	Leu	Ser	Ala	Trp	Gly	Val	Ile	Met	Leu
			20					25					30		
Ile	Met	Leu	Gly	Ile	Phe	Phe	Asn	Val	His	Ser	Ala	Val	Xaa	Ile	Xaa
			35				40					45			
Asp	Val	Pro	Phe	Thr	Glu	Lys	Asp	Phe	Glu	Asn	Gly	Pro	Gln	Asn	Ile
			50			55					60				
Tyr	Asn	Leu	Tyr	Glu	Gln	Val	Ser	Tyr	Asn	Cys	Phe	Ile	Ala	Ala	Gly
65					70					75					80
Leu	Tyr	Leu	Leu	Xaa	Gly	Gly	Phe	Ser	Phe	Cys	Gln	Val	Arg	Leu	Asn
				85					90					95	

Lys Arg Lys Glu Tyr Met Val Arg
100

<210> 170
<211> 123
<212> PRT
<213> Rat

<220>
<221> UNSURE
<222> (27)...(27)

<221> UNSURE
<222> (104)...(104)

<221> UNSURE
<222> (118)...(118)

<400> 170
Met Arg Pro Gly Ala Asp Trp Ala Ala Val Cys Ala Leu Trp Pro Ser
1 5 10 15
Trp Arg Pro Ser Cys Ser Leu Pro Ser Ser Xaa Arg Ile Gln Pro Asp
20 25 30
Glu Leu Trp Leu Tyr Arg Asn Pro Tyr Val Lys Ala Glu Tyr Phe Pro
35 40 45
Thr Gly Pro Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile
50 55 60
Phe Phe Ala Lys Phe Leu Arg Lys Ala Asp Ala Asp Arg Gln Arg Ala
65 70 75 80
Ser Leu Pro Arg Cys Gln Pro Cys Pro Ser Ala Lys Trp Cys Leu Tyr
85 90 95
Gln His His Lys Thr Asp Ser Xaa Gln Gly His Ala Gln Ile Ala Ser
100 105 110
Thr Glu Cys Ser Pro Xaa Gly Ile Ala His Ser
115 120

<210> 171
<211> 75
<212> PRT
<213> Rat

<400> 171
Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
1 5 10 15
Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
20 25 30
Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
35 40 45
Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
50 55 60
Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
65 70 75

<210> 172
<211> 79
<212> PRT
<213> Human

<400> 172
Lys Thr Ser Tyr His Tyr His Thr Asn Val Glu Glu Leu Thr Ile Pro
1 5 10 15

Glu Thr Arg Asn Asn Leu Tyr Ile Ser Ile Ser Trp Leu Trp Cys Leu
 20 25 30
 Val Leu Val Leu Leu Ser Thr Met Ile Leu Asn Lys His Gly Trp Met
 35 40 45
 Lys Ala Asn Ala Tyr Ser Leu Val Pro Ser Ile Ile Tyr Ser Pro Ser
 50 55 60
 Tyr Leu Lys Leu Leu Leu Arg Leu Tyr Lys Leu Gln Ile Cys Cys
 65 70 75

<210> 173
 <211> 134
 <212> PRT
 <213> Human

<220>
 <400> 173
 Leu Arg Gly Arg Gly Arg Gly Val Cys Ser Gln Glu Ser Phe Gly Gly
 1 5 10 15
 Cys Cys Val Ser Gly Leu Ile Ala Met Gly Thr Lys Ala Gln Val Glu
 20 25 30
 Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu
 35 40 45
 Ala Leu Gly Ser Val Thr Val His Ser Ser Glu Pro Glu Val Arg Ile
 50 55 60
 Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser
 65 70 75 80
 Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu
 85 90 95
 Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr
 100 105 110
 Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr
 115 120 125
 Gly Thr Tyr Thr Cys Met
 130

<210> 174
 <211> 137
 <212> PRT
 <213> Human

<400> 174
 Ala Trp Ser Arg Pro Arg Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala
 1 5 10 15
 Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe
 20 25 30
 Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly
 35 40 45
 Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile
 50 55 60
 Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr
 65 70 75 80
 Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn
 85 90 95
 Ile Lys Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser
 100 105 110
 Ala Leu Val Ile Leu Gly Gly Ala Leu Ser Pro Val Pro Val Leu Gly
 115 120 125
 Ile Arg Ala Gly Leu Gly Thr Cys Pro
 130 135

<210> 175

<211> 43
 <212> PRT
 <213> Human

<400> 175
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
 1 5 10 15
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
 20 25 30
 Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
 35 40

<210> 176
 <211> 63
 <212> PRT
 <213> Rat

<400> 176
 Pro Asn Thr Arg Pro Arg Arg His Thr Ala Cys Arg Val Ser Ile Ser
 1 5 10 15
 Val Phe Tyr Met Leu His Thr Glu Leu Lys Lys Cys Trp Phe Phe Leu
 20 25 30
 Phe Cys Phe Ser Leu Phe Leu Trp Phe Cys Phe Trp Phe Cys Phe Leu
 35 40 45
 Leu Pro Arg Phe Asp Tyr Leu Pro Met Pro Ser Thr Arg Pro Arg
 50 55 60

<210> 177
 <211> 52
 <212> PRT
 <213> mouse

<400> 177
 Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
 1 5 10 15
 Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
 20 25 30
 Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
 35 40 45
 Gly Ala Gln Gly
 50

<210> 178
 <211> 62
 <212> PRT
 <213> mouse

<400> 178
 Val Ser Pro Arg Pro Thr Tyr Pro Ser Thr Ala Ser Ser Met Ala Ala
 1 5 10 15
 Phe Leu Val Thr Gly Phe Phe Phe Ser Leu Phe Val Val Leu Gly Met
 20 25 30
 Glu Pro Arg Ala Leu Phe Arg Pro Asp Lys Ala Leu Pro Leu Ser Cys
 35 40 45
 Ala Lys Pro Thr Ser Leu Cys Val Gln Ser Ser Phe Leu Gly
 50 55 60

<210> 179
 <211> 123
 <212> PRT
 <213> mouse

<400> 179

Ala	Ser	Arg	Thr	Ala	Val	Met	Ser	Leu	Cys	Arg	Cys	Gln	Gln	Gly	Ser
1				5					10					15	
Arg	Ser	Arg	Met	Asp	Leu	Asp	Val	Val	Asn	Met	Phe	Val	Ile	Ala	Gly
			20					25					30		
Gly	Thr	Leu	Ala	Ile	Pro	Ile	Leu	Ala	Phe	Val	Ala	Ser	Phe	Leu	Leu
		35					40					45			
Trp	Pro	Ser	Ala	Leu	Ile	Arg	Ile	Tyr	Tyr	Trp	Tyr	Trp	Arg	Arg	Thr
	50					55					60				
Leu	Gly	Met	Gln	Val	Arg	Tyr	Ala	His	His	Glu	Asp	Tyr	Gln	Phe	Cys
65				70						75					80
Tyr	Ser	Phe	Arg	Gly	Arg	Pro	Gly	His	Lys	Pro	Ser	Ile	Leu	Met	Leu
			85						90				95		
His	Gly	Phe	Ser	Ala	His	Lys	Gly	His	Val	Ala	Gln	Arg	Gly	Gln	Val
			100				105						110		
Pro	Ser	Arg	Lys	Asn	Leu	His	Phe	Gly	Cys	Val					
		115					120								

<210> 180

<211> 120

<212> PRT

<213> mouse

<220>

<221> UNSURE

<222> (5) ... (5)

<400> 180

Ala	Arg	Arg	Arg	Xaa	Arg	Trp	Arg	Arg	Gly	Cys	Cys	Trp	Leu	Ile	Gly
1				5					10					15	
Thr	Gly	Leu	Arg	Ala	Ala	Thr	Trp	Thr	Val	Leu	Cys	Ser	Pro	Asn	Ser
			20					25					30		
Ser	Leu	Val	Val	Ala	Arg	His	Thr	Lys	Ser	Phe	Pro	Pro	Lys	Lys	Pro
		35					40					45			
Leu	Gln	Ala	Leu	Thr	Met	Ser	Ile	Met	Asp	His	Ser	Pro	Thr	Thr	Gly
	50					55					60				
Val	Val	Thr	Val	Ile	Val	Ile	Leu	Ile	Ala	Ile	Ala	Ala	Leu	Gly	Gly
65				70					75						80
Leu	Ile	Leu	Gly	Cys	Trp	Cys	Tyr	Leu	Arg	Leu	Gln	Arg	Ile	Ser	Gln
			85					90					95		
Ser	Glu	Asp	Glu	Glu	Ser	Ile	Val	Gly	Asp	Gly	Glu	Thr	Lys	Glu	Pro
		100					105						110		
Phe	Tyr	Trp	Cys	Ser	Thr	Leu	Leu								
		115					120								

<210> 181

<211> 60

<212> PRT

<213> mouse

<400> 181

Lys	Gly	Pro	Glu	Val	Ser	Cys	Cys	Ile	Lys	Tyr	Phe	Ile	Phe	Gly	Phe
1				5					10					15	
Asn	Val	Ile	Phe	Trp	Phe	Leu	Gly	Ile	Thr	Phe	Leu	Gly	Ile	Gly	Leu
		20					25						30		
Trp	Ala	Trp	Asn	Glu	Lys	Gly	Val	Leu	Ser	Asn	Ile	Ser	Ser	Ile	Thr
	35					40						45			
Asp	Leu	Gly	Gly	Phe	Asp	Pro	Val	Trp	Leu	Phe	Leu				
	50					55					60				

<210> 182
 <211> 72
 <212> PRT
 <213> mouse

<220>

<400> 182
 Lys Pro Thr Val Gly Ser Ala Glu Val Ala Ile Ala Val Phe Leu Val
 1 5 10 15
 Ile Cys Ile Ile Val Val Leu Thr Ile Leu Gly Tyr Cys Phe Phe Lys
 20 25 30
 Asn Gln Arg Lys Glu Phe His Ser Pro Leu His His Pro Pro Pro Thr
 35 40 45
 Pro Ala Ser Ser Thr Val Ser Thr Thr Glu Asp Thr Glu His Leu Val
 50 55 60
 Tyr Asn His Thr Thr Gln Pro Leu
 65 70

<210> 183
 <211> 771
 <212> PRT
 <213> Rat

<220>

<400> 183
 Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu Leu
 1 5 10 15
 Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg Ile
 20 25 30
 Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu Thr
 35 40 45
 Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr Phe
 50 55 60
 Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp Ile
 65 70 75 80
 Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu Ser Ala Leu Ser His
 85 90 95
 Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln Trp
 100 105 110
 Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala Arg
 115 120 125
 Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr Pro
 130 135 140
 Ser Lys Asn Phe Thr Cys Gln Gly Pro Val Asp Val Thr Ile Gln Ala
 145 150 155 160
 Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr Cys
 165 170 175
 Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly Phe
 180 185 190
 Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Thr Ser Asn Pro
 195 200 205
 Cys Lys His Gly Gly Thr Cys His Leu Lys Pro Arg Arg Glu Thr Trp
 210 215 220
 Ile Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly Glu Ser Cys Asp Ile
 225 230 235 240
 Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr Cys
 245 250 255

Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr Thr
 260 265 270
 Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu Asn
 275 280 285
 Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe Lys
 290 295 300
 Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His Cys Asp Ile Asp Phe
 305 310 315 320
 Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr Asp
 325 330 335
 Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu Gly Tyr Ser Gly Leu
 340 345 350
 Phe Cys Glu Phe Ser Pro Pro Met Val Phe Leu Arg Thr Ser Pro Cys
 355 360 365
 Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Ile Arg Val Asn
 370 375 380
 Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu Gly Glu Lys Cys Glu
 385 390 395 400
 Lys Leu Val Ser Val Ser Ile Leu Val Asn Lys Glu Ser Tyr Leu Gln
 405 410 415
 Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile
 420 425 430
 Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp
 435 440 445
 His Ile Ala Val Glu Ser Ile Glu Gly Ile Arg Ala Ser Tyr Asp Thr
 450 455 460
 Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn Asp
 465 470 475 480
 Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu Asp Ser Ser Leu Ser
 485 490 495
 Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile Thr Asn Leu Ser Lys
 500 505 510
 Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met Pro
 515 520 525
 Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn Gly
 530 535 540
 Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu Leu
 545 550 555 560
 Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly Ile Leu Pro Gly Cys
 565 570 575
 Glu Pro Cys His Lys Lys Val Cys Ala His Gly Thr Cys Gln Pro Ser
 580 585 590
 Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu Gly Trp Met Gly Pro
 595 600 605
 Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys Val
 610 615 620
 His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys Cys
 625 630 635 640
 Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu Phe
 645 650 655
 Asn Pro Leu Pro Gly Asp Gln Val Gln Ala Arg Glu Val Gln Ala Leu
 660 665 670
 Trp Ala Arg Ala Ala Leu Leu Trp Met Gln Gln Trp Ile His Arg Gly
 675 680 685
 Gln Leu Thr Gln Arg Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp Tyr
 690 695 700
 Tyr Gln Ser Ser Arg Val Arg Cys Leu Ser Asn Asp

<210> 184

<211> 340

<212> PRT

<213> mouse

<400> 184

Asp Gly Ser Leu Trp Leu Gln Ala Thr Gln Pro Asp Asp Ala Gly His
 1 5 10 15
 Tyr Thr Cys Val Pro Ser Asn Gly Phe Leu His Pro Pro Ser Ala Ser
 20 25 30
 Ala Tyr Leu Thr Val Leu Tyr Pro Ala Gln Val Thr Val Met Pro Pro
 35 40 45
 Glu Thr Pro Leu Pro Thr Gly Met Arg Gly Val Ile Arg Cys Pro Val
 50 55 60
 Arg Ala Asn Pro Pro Leu Leu Phe Val Thr Trp Thr Lys Asp Gly Gln
 65 70 75 80
 Ala Leu Gln Leu Asp Lys Phe Pro Gly Trp Ser Leu Gly Pro Glu Gly
 85 90 95
 Ser Leu Ile Ile Ala Leu Gly Asn Glu Asp Ala Leu Gly Glu Tyr Ser
 100 105 110
 Cys Thr Pro Tyr Asn Ser Leu Gly Thr Ala Gly Pro Ser Pro Val Thr
 115 120 125
 Arg Val Leu Leu Lys Ala Pro Pro Ala Phe Ile Asp Gln Pro Lys Glu
 130 135 140
 Glu Tyr Phe Gln Glu Val Gly Arg Glu Leu Leu Ile Pro Cys Ser Ala
 145 150 155 160
 Arg Gly Asp Pro Pro Pro Ile Val Ser Trp Ala Lys Val Gly Arg Gly
 165 170 175
 Leu Gln Gly Gln Ala Gln Val Asp Ser Asn Asn Ser Leu Val Leu Arg
 180 185 190
 Pro Leu Thr Lys Glu Ala Gln Gly Arg Trp Glu Cys Ser Ala Ser Asn
 195 200 205
 Ala Val Ala Arg Val Thr Thr Ser Thr Asn Val Tyr Val Leu Gly Thr
 210 215 220
 Ser Pro His Val Val Thr Asn Val Ser Val Val Pro Leu Pro Lys Gly
 225 230 235 240
 Ala Asn Val Ser Trp Glu Pro Gly Phe Asp Gly Gly Tyr Leu Gln Arg
 245 250 255
 Phe Ser Val Trp Tyr Thr Pro Leu Ala Lys Arg Pro Asp Arg Ala His
 260 265 270
 His Asp Trp Val Ser Leu Ala Val Pro Ile Gly Ala Thr His Leu Leu
 275 280 285
 Val Pro Gly Leu Gln Ala His Ala Gln Tyr Gln Phe Ser Val Leu Ala
 290 295 300
 Gln Asn Lys Leu Gly Ser Gly Pro Phe Ser Glu Ile Val Leu Ser Ile
 305 310 315 320
 Pro Glu Gly Leu Pro Thr Thr Pro Ala Ala Pro Gly Leu Pro Ala Thr
 325 330 335
 Arg Ser Arg Val
 340

<210> 185

<211> 536

<212> PRT

<213> mouse

<400> 185

Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
 1 5 10 15
 Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
 20 25 30
 Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
 35 40 45
 Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg

50	55	60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg		
65	70	75
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val		80
	85	90
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu		95
	100	105
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val		110
	115	120
Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp		125
	130	135
Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr Gln Met Ser Arg		140
145	150	155
Phe Leu Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His		160
	165	170
Asp Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Gly Tyr Leu Pro Pro		175
	180	185
Glu Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val		190
	195	200
Tyr Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Asn Asn Pro		205
	210	215
Phe Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys		220
225	230	235
Gly His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala		240
	245	250
Cys Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro		255
	260	265
Gln Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu		270
	275	280
Cys Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly		285
	290	295
Glu Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser		300
305	310	315
Arg Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu		320
	325	330
Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Phe Pro Arg Leu Leu		335
	340	345
Lys Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro		350
	355	360
Ser Ser Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser		365
	370	375
Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala		380
385	390	395
Ser Thr Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val		400
	405	410
Asp Ala Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln		415
	420	425
Pro Gln Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His		430
	435	440
Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu		445
	450	455
Asn Asn Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu		460
465	470	475
His Met Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu		480
	485	490
Ala Arg Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala		495
	500	505
Leu His Phe Ala Ala Gln Asn Gly Asp Glu Gly Gln His Lys Ala Ala		510
	515	520
Ala Arg Glu Glu Cys Phe Cys Gln		525
530	535	

<210> 186
 <211> 337
 <212> PRT
 <213> Rat

<220>

<400> 186

Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp
 1 5 10 15
 Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile
 20 25 30
 Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr
 35 40 45
 Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly
 50 55 60
 Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr
 65 70 75 80
 Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp
 85 90 95
 Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn
 100 105 110
 Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu
 115 120 125
 Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
 130 135 140
 Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys
 145 150 155 160
 Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser Cys Gln
 165 170 175
 Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro Leu Gln
 180 185 190
 Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Val
 195 200 205
 Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met Cys Pro
 210 215 220
 Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Phe Arg
 225 230 235 240
 Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln
 245 250 255
 Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile
 260 265 270
 Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro
 275 280 285
 Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp
 290 295 300
 Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe
 305 310 315 320
 Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro
 325 330 335
 Phe

<210> 187
 <211> 152
 <212> PRT
 <213> mouse

<400> 187

Met Ala Leu Gly Val Leu Ile Ala Val Cys Leu Leu Phe Lys Ala Met
 1 5 10 15
 Lys Ala Ala Leu Ser Glu Glu Ala Glu Val Ile Pro Pro Ser Thr Ala
 20 25 30
 Gln Gln Ser Asn Trp Thr Phe Asn Asn Thr Glu Ala Asp Tyr Ile Glu
 35 40 45
 Glu Pro Val Ala Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn
 50 55 60
 Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln
 65 70 75 80
 Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His
 85 90 95
 Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile Ala
 100 105 110
 Ile Gly Ile Gly Val Gly Leu Leu Ile Ser Ala Phe Leu Ala Val Phe
 115 120 125
 Tyr Cys Tyr Ile Arg Lys Arg Cys Ile Asn Leu Lys Ser Pro Tyr Ile
 130 135 140
 Ile Cys Ser Gly Gly Ser Pro Leu
 145 150

<210> 188

<211> 118

<212> PRT

<213> Rat

<220>

<400> 188

Leu Val Pro Gln Phe Gly Thr Arg Ile Arg Tyr ThrAla Tyr Asp Arg
 1 5 10 15
 Ala Tyr Asn Arg Ala Ser Cys Lys Phe Ile Val Lys Val Gln Val Arg
 20 25 30
 Arg Cys Pro Ile Leu Lys Pro Pro Gln His Gly Tyr Leu Thr Cys Ser
 35 40 45
 Ser Ala Gly Asp Asn Tyr Gly Ala Ile Cys Glu Tyr His Cys Asp Gly
 50 55 60
 Gly Tyr Glu Arg Gln Gly Thr Pro Ser Arg Val Cys Gln Ser Ser Arg
 65 70 75 80
 Gln Trp Ser Gly Ser Pro Pro Val Cys Thr Pro Met Lys Ile Asn Val
 85 90 95
 Asn Val Asn Ser Ala Ala Gly Leu Leu Asp Gln Phe Tyr Glu Lys Gln
 100 105 110
 Arg Leu Leu Ile Val Ser
 115

<210> 189

<211> 299

<212> PRT

<213> Human

<220>

<400> 189

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe

50	55	60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr		
65	70	75
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe		80
	85	90
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser		95
	100	105
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val		110
	115	120
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr		125
	130	135
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro		140
145	150	155
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn		160
	165	170
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro		175
	180	185
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly		190
	195	200
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser		205
	210	215
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val		220
225	230	235
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly		240
	245	250
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly		255
	260	265
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu		270
	275	280
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val		285
290	295	

<210> 190
 <211> 91
 <212> PRT
 <213> Human

<400> 190
Gln Pro Thr Val Phe Trp Pro Lys Thr Ser Ala Lys Lys Gly Asn Trp
1 5 10 15
Val Leu Arg Leu Gly Leu Ser Asn Pro Asp Arg Pro Ala Arg Gln Asn
20 25 30
Asn Trp Phe Leu Pro Ala Ser Arg Glu Ile Pro Glu His Ser Ala Leu
35 40 45
Thr Arg Tyr Pro Ala Gln Ile Arg Gly Cys Trp Pro His Arg Leu Thr
50 55 60
Lys Pro Gln Thr Cys Leu Pro Gln Ala Arg Ser Tyr Leu Ser His Glu
65 70 75 80
Val Thr Gln Ala Thr Arg Thr Cys Pro Gly Gly
85 90

<210> 191
 <211> 89
 <212> PRT
 <213> mouse

<400> 191
Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu Asp
1 5 10 15
Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly Lys
20 25 30

Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr Ala
 35 40 45
 Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr Pro
 50 55 60
 Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr Pro
 65 70 75 80
 Cys Gln Pro Gly Gln Arg Val Glu Val
 85

<210> 192
 <211> 299
 <212> PRT
 <213> mouse

<220>

<400> 192
 Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
 1 5 10 15
 Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
 20 25 30
 Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr
 35 40 45
 Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
 50 55 60
 Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg
 65 70 75 80
 Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
 85 90 95
 Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
 100 105 110
 Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
 115 120 125
 Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
 130 135 140
 Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
 145 150 155 160
 Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
 165 170 175
 Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
 180 185 190
 Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys
 195 200 205
 Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
 210 215 220
 Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
 225 230 235 240
 Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
 245 250 255
 Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
 260 265 270
 Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
 275 280 285
 Pro Gln His Ser Ser Ser Lys Ala Met Lys His
 290 295

<210> 193
 <211> 314
 <212> PRT
 <213> mouse

<220>

<400> 193

Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn Ile Asp
 1 5 10 15
 Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met
 20 25 30
 Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile
 35 40 45
 Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr
 50 55 60
 Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly
 65 70 75 80
 Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His
 85 90 95
 Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys
 100 105 110
 Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln
 115 120 125
 Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser
 130 135 140
 Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr
 145 150 155 160
 Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu
 165 170 175
 Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly
 180 185 190
 Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu
 195 200 205
 Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly
 210 215 220
 Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg
 225 230 235 240
 Cys Val Asp Thr SerGln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala
 245 250 255
 Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly
 260 265 270
 Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln
 275 280 285
 Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe
 290 295 300
 Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
 305 310

<210> 194

<211> 109

<212> PRT

<213> mouse

<400> 194

Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
 1 5 10 15
 Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
 20 25 30
 Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
 35 40 45
 Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
 50 55 60
 Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
 65 70 75 80
 Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr

85 90 95
 Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
 100 105

<210> 195
 <211> 237
 <212> PRT
 <213> mouse

<400> 195
 Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1 5 10 15
 Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
 20 25 30
 Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
 35 40 45
 Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
 50 55 60
 Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
 65 70 75 80
 Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
 85 90 95
 Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
 100 105 110
 Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
 115 120 125
 Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
 130 135 140
 Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
 145 150 155 160
 Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
 165 170 175
 Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
 180 185 190
 Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
 195 200 205
 Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu
 210 215 220
 His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe
 225 230 235

<210> 196
 <211> 154
 <212> PRT
 <213> Human

<400> 196
 Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
 1 5 10 15
 Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
 20 25 30
 Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala His Asn Ile
 35 40 45
 Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
 50 55 60
 Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
 65 70 75 80
 Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu
 85 90 95
 His Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile
 100 105 110

Ala Ile Gly Ile Gly Val Gly Leu Leu Leu Ser Gly Phe Leu Val Ile
 115 120 125
 Phe Tyr Cys Tyr Ile Arg Lys Arg Cys Leu Lys Leu Lys Ser Pro Tyr
 130 135 140
 Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
 145 150

<210> 197

<211> 171

<212> PRT

<213> Rat

<400> 197

Met Ala Arg Pro Ala Pro Trp Trp Trp Leu Arg Pro Leu Ala Ala Leu
 1 5 10 15
 Ala Leu Ala Leu Ala Leu Val Arg Val Pro Ser Ala Arg Ala Gly Gln
 20 25 30
 Met Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr Glu
 35 40 45
 Glu Glu Leu Ala Arg Tyr Ser Gly Glu Glu Glu Asp Gln Pro Ile Tyr
 50 55 60
 Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu Phe
 65 70 75 80
 Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Ala Gly Lys Asp Ser Ser
 85 90 95
 Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His Asp
 100 105 110
 Ile Ser Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Asp Ile Phe
 115 120 125
 Ser Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala Arg
 130 135 140
 Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro Glu
 145 150 155 160
 Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
 165 170

<210> 198

<211> 1399

<212> DNA

<213> Mouse

<400> 198

ggcaaagact tcggcacgag asaacagcaa agcagagctg gctgcagcca ttcactggcc 60
 tcgggcgggc gtgccacaga ggcagttgaa gtgaaagtga aagagaaacg ataagagaac 120
 ggagaccaca ggtgctaagt gaggggtgctc acagaacccc ctcttcagcc agagatcact 180
 agcaggggaa ctgtggagaa ggcagccagc aaggaagagc ctgagagtag cctccatggg 240
 cttggagccc agctggatc tgetgctctg tttggctgtc tctggggcag cagggactga 300
 ccctcccaca gcgcccacca cagcagaaag acagcggcag cccacggaca tcatcttaga 360
 ctgcttcttg gtgacagaag acaggcaccg cggggctttt gccagcagtg gggacaggga 420
 gagggccttg cttgtgctga agcaggtacc agtgtctgat gatggctccc tggaaggcat 480
 cacagatttc caggggagca ctgagaccaa acaggattca cctgttatct ttgaggcctc 540
 agtggacttg gtacagattc cccaggcaga ggcgttgctc catgctgact gcagcgggaa 600
 ggcagtgacc tgcgagatct ccaagtattt cctccaggcc agacaagagg ccacttttga 660
 gaaagcacat tggttcatca gcaacatgca ggtttctaga ggtggcccca gtgtctccat 720
 ggtgatgaag actctaagag atgctgaagt tggagctgtc cggcacccta cactgaacct 780
 acctctgagt gcccagggca cagtgaagac tcaagtggag ttccagggtga catcagagac 840
 ccaaaccctg aaccacctgc tggggctctc tgtctccctg cactgcagtt tctccatggc 900
 accagacctg gacctcactg gcgtggagtg gcggctgcag cataaaggca gcggccagct 960
 ggtgtacagc tggaagacag ggcaggggca ggccaagcgc aagggcgcta cactggagcc 1020
 tgaggagcta ctcagggtg gaaacgcctc tctcacctta cccaacctca ctctaaagga 1080
 tgaggggacc tacatctgcc agatctccac ctctctgtat caagctcaac agatcatgcc 1140

acttaacatc	ctggctcccc	ccaaagtaca	actgcacttg	gcaaacaagg	atcctctgcc	1200
tcccctcgtc	tgacgacattg	cgggctacta	tcctctggat	gtgggagtga	cgtggattcg	1260
agaggagctg	ggtggaattc	cagcccaagt	ctctggtgcc	tccttctcca	gcctcaggca	1320
gagcacgatg	ggaacctaca	gcatttcttc	cacgggtgatg	gctgaccacg	gccccacagg	1380
tgccacttat	acctgccaa					1399

<210> 199

<211> 469

<212> DNA

<213> Rat

<400> 199

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gaaatggcag	caaataaagc	tctcaaaact	cacagagaat	aaaggaaggc	agcaggagaa	300
gggtctccag	agatatcgct	gggtctgctg	gctcctgtgc	tgtacctg	tgctatccag	360
acccttagg	caactgcaga	gggcttggtg	tgggggactg	gagtaccatg	atgctcccag	420
ggtgagcctc	cactgcctc	agccttgctc	ccaacagcgt	cagggtactg		469

<210> 200

<211> 529

<212> DNA

<213> Rat

<400> 200

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ccagacagac	agtatgtgct	gacagccttg	gctgcgcggg	ccaagcttag	agcctggaat	180
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caggaatatg	tcaatctggt	ggaagatgtg	gacacaaagt	tgaacttagc	cactaagttc	360
aagtgccatg	atgttgatc	tgatacttgc	cgagacctga	aggatcgctc	acagttgctt	420
gcatacagga	gcaaagtaga	ttaaaggatc	gctgaggaag	agaaaatcga	tgtcatcctc	480
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<210> 201

<211> 1230

<212> DNA

<213> Rat

<400> 201

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ggcgcccgcc	aggctgctac	cgagctgcgc	gctcttccag	gacctcatcc	gctacgggaa	180
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aagtacactt	tctgcagctg	gcgcccgcga	ggctgctacc	gagctgcgcg	ctcttccagg	1140
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cgggggatcc	actagttcta	gagcgccgcc				1230

<210> 202

<211> 778

<212> DNA

<213> Rat

<400> 202

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aaatgaaatg	gaaaacattt	attacacaaa	tttaattaca	attctaggga	ataaacatgc	180
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cactgttgta	aagaacagcg	tcacatttag	cgcactctggc	gtagtagcag	tttttaacac	360
tttgccgagg	tgctccctt	ccccaccgcg	cgctttgtta	ggctctacct	tctaaatctc	420
tgcttctctc	gcacagtaag	tgacctctcc	atgacaaagg	gccccagac	agcagttata	480
aatcaatgtg	ttttgggttt	gtttgtttgt	ttgtttgttt	ttaaagaaaa	acccggccat	540
gcttggtggc	acttgccctt	aatagtagcg	cttggttagac	agaggcaagc	ggttctctgt	600
aagttcaagg	ccagcctggg	ctacacagtg	agaccgggtc	tcaaaaacaa	aacaacaaaa	660
aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	gatcactgtc	tgcaactaa	720
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<210> 203

<211> 1123

<212> DNA

<213> Rat

<400> 203

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cgggtgccta	cagcccccat	cagcttcccc	ggggagattc	tgccgatttg	tcacgagcca	180
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ctcctggcat	tccaggaaac	catggaaaca	atggaaataa	cggagccact	ggccacgaag	420
gggccaaagg	tgagaaagga	gacaaaggcg	acctggggcc	tcgaggggaa	cgggggcagc	480
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<210> 204

<211> 434

<212> DNA

<213> Mouse

<400> 204

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agagatgaaa	tttttgctaa	acttcaaccg	aagcttagat	gcacattagg	tgacatggaa	180
agtcctgtgt	ttgcacttcc	tgtactgtta	aagcttgaac	cccatgttga	aagcctcttt	240
acatattctt	tttcttgga	ttttgaatgt	tcccattgtg	gacaccagta	ccaaaacagg	300

tgtgtgaaga	gtctgggtcac	ctttaccaat	attgttcctg	agtggcatcc	actcaatgct	360
gcccattttg	gtccatgtaa	cagctgcaac	agtaaatacac	aaataagaaa	aatgggtgtg	420
gaaagagcgt	cgcc					434

<210> 205
 <211> 783
 <212> DNA
 <213> Mouse

<400> 205						
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cgtggatcaa	ctcatggagc	tggccggggt	gagctgtgcc	acggctattg	ccaaggctta	300
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gaaaatggac	attcctttcc	ttggtgaaat	gccccagag	gatgggatgt	agagaaggga	540
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actcacttta	ctggccgata	tcattacctt	gggggtcgct	ttgtaccacc	tgctctagag	660
aagaagtacc	agctgaacct	gccatcttac	cctgacacag	agtgtgtcta	ccgtctacag	720
taagggaggt	gggtaggcag	gattctcaat	aaagacttgg	tactttctgt	cttgaaaaaa	780
aaa						783

<210> 206
 <211> 480
 <212> DNA
 <213> Mouse

<400> 206						
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tagtaacaag	ataccatgca	gctccctcta	gcctcggatc	accgaagcag	gaagaaggtc	180
agactgcccc	catcccagat	ttgcttagtt	tgtctcccaa	tgtgctggac	tttaaagaca	240
gggaatggag	aagcagatgg	atgcttcagt	ttcagtcatt	tttggctcta	tagtgatctc	300
tgctttctctg	tacctgtcct	tggctggacc	ctgggcagta	actgtcactc	agatgaggac	360
gatcatcatt	acaatggacc	aactgaggga	tgccctcata	ttagaccaat	taaaagttgc	420
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<210> 207
 <211> 501
 <212> DNA
 <213> Mouse

<400> 207						
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agtattggag	tttgggggtg	a				501

<210> 208
 <211> 480
 <212> DNA
 <213> Mouse

<400> 208

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ctgttgcttt	tgcattgtta	atatagacgt	tcctgtcgat	ccttgggaga	tcattggcctt	420
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<210> 209

<211> 962

<212> DNA

<213> Mouse

<400> 209

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aaatgatgcc	acagaaatcc	tttattcaca	tgtgggttaa	cctgtcccgg	cacaccccag	180
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aatgagtggg	ttgcagtga	agccaggcat	cctgtagttt	ccatcccctc	ccccatccca	900
gtcatttctt	taaaagcacc	tgatgctgca	ttctgttaca	gtttaaaaaa	aaaaaaaaaa	960
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<210> 210

<211> 778

<212> DNA

<213> Mouse

<400> 210

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gtaccagctg	aacctgccat	cttaccctga	cacagagtgt	gtctaccgtc	tacagtaagg	720
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<210> 211

<211> 1152

<212> DNA

<213> Mouse

<400> 211

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<210> 212

<211> 446

<212> DNA

<213> Mouse

<400> 212

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actcctggag	ctggagttag	agacaatggt	gagctgcctt	gtggatgttg	ggaattgaac	180
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ctaatataga	ttatttatga	attcaggtgg	cttaatggta	tatgcatgaa	ttagtagtaa	360
aacaagaact	agggccagca	agtggcttaa	gggtgcctgc	taaccatctc	agccacctga	420
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<210> 213

<211> 2728

<212> DNA

<213> Mouse

<400> 213

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<210> 214

<211> 2046

<212> DNA

<213> Rat

<400> 214

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<210> 215

<211> 493

<212> DNA

<213> Mouse

<400> 215

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<210> 216

<211> 511

<212> DNA

<213> Mouse

<400> 216

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<210> 217

<211> 1107

<212> DNA

<213> Rat

<400> 217

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<210> 218
 <211> 1001
 <212> DNA
 <213> Rat

<400> 218						
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 <211> 2206
 <212> DNA
 <213> Rat

<400> 219						
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<210> 220

<211> 376

<212> DNA

<213> Human

<400> 220

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<210> 221

<211> 433

<212> DNA

<213> Human

<400> 221

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<210> 222

<211> 530

<212> DNA

<213> Human

<400> 222

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<210> 223

<211> 550

<212> DNA

<213> Mouse

<400> 223

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<210> 224

<211> 470

<212> DNA

<213> Mouse

<400> 224

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<210> 225

<211> 1752

<212> DNA

<213> Rat

<400> 225

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<210> 226
 <211> 2165
 <212> DNA
 <213> Mouse

<400> 226

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<210> 227
 <211> 1348
 <212> DNA
 <213> Mouse

<220>
 <221> unsure
 <222> (644) ... (644)

<400> 227

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<210> 228

<211> 2296

<212> DNA

<213> Mouse

<220>

<221> unsure

<222> (2255) ... (2255)

<400> 228

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aatagctatt	tcacagcagt	aacagaagct	acctgctata	ataaagacct	caacactgct	180
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<210> 229

<211> 1704

<212> DNA

<213> Rat

<220>

<400> 229

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<210> 230

<211> 2004

<212> DNA

<213> Rat

<400> 230

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<210> 231

<211> 1397

<212> DNA

<213> Rat

<400> 231

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gtgtcttgga	gccaccccaa	ggcaggggtca	tcctggcctt	ggttttgccc	tttcatccct	1020
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agaattggga	agagcaagtg	aatagcctgc	ctgaggtgtt	caggaaagct	ggctttgtca	1140
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agagtcaccc	ctggaatctg	ccctccagaa	gaggaggtgc	atccagtgat	gtgaggggga	1320
cctctgggga	ctgtcattct	cagtatcatg	taggaattta	aaaagccaaa	atactaattc	1380
tttctttgta	gtgtgta					1397

<210> 232

<211> 861

<212> DNA

<213> Rat

<400> 232

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ttagcaccta	gcttgtttgt	gtctgataca	ccaccaagta	gtaattggtg	aaaaaacgaa	120
gaagaaaaaa	aaaaaacaaa	aaaaccaaac	agtgggtact	caaataagat	aggagaaaaa	180
tgagagaaca	gacccagttc	tcgacccttg	cttctcaagg	tcctcccacc	aggctgccaa	240
agcaagatgg	tgttgctctg	atccagtcag	tattcttttg	actttttttt	ttaatctcca	300
ggttttgggt	caggctccca	tattcatacc	ctggctcatt	tagctttccc	tcattgtgtg	360
ggttcttctg	tccttcaccc	ccttactctc	cccactgata	ttcttcccag	tcaagactgt	420
ggctctggaa	gaaatatcca	ccattttgcag	agctgatgtt	ctgtagatcg	taatgttgaa	480
gcgctgggtg	tcctgggttg	cagaatcact	cctgtattac	tctggtacat	agggtgtctc	540
tgatagactc	cctggcctta	gtcatggggt	gttttctaga	ggcagactaa	gacaggagtc	600
aaaaaagatt	tagaggaagg	agctgaggaa	agaaagacag	ttgtgggagg	aaaatcaagt	660
tctactcagg	atcccagagt	tttctgtaga	tgtagattgg	aatgtgtcca	taacagagag	720
gccagtgaga	gacatcccca	aggacctgcc	aggctttcct	tcgctccagg	aagacgcacc	780
atcactcaaa	aggggtttcc	tagaaagaaa	gacaagtgac	ttaaaaaatc	tgccagtggg	840
ttcttgaagt	catcgaacct	a				861

<210> 233

<211> 445

<212> DNA

<213> Mouse

<400> 233

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gctggtggcc	gcactgtggg	gtggcacgca	gccgctgctg	aagcgagcct	cctccggcct	120
ggagcaagtg	cgtgagcggg	cgtgggcctg	gcagctgttg	caggagataa	aggctctctt	180
cgggaatact	gaggtgcgtc	tagctctcac	ggacgagccc	ctgaaaattt	caccataggt	240
cggccgtatt	cccagcccat	ctcttactca	ctagaagtcc	ctggaagagt	catttatcct	300
cttacctgat	gccctttctc	ctcaatcaga	gtggatccct	tctctactac	ttgactttgg	360
catcaacaga	tctgacgtta	gctgtgcccc	tctgcaactc	tctggccatc	gtctttacac	420
tgattgttgg	gaaggctcct	ggaga				445

<210> 234

<211> 565

<212> DNA

<213> Human

<400> 234

cagcatcctc	aatcaatcca	acagcatatt	cggttgcatc	ttctacacac	tacagctatt	60
gttaggttgc	ctgcggacac	gctgggcctc	tgtcctgatg	ctgctgagct	ccctgggtgc	120
tctcgtgggt	tctgtctacc	tggcctggat	cctgttcttc	gtgctctatg	atttctgcat	180
tgtttgtatc	accacctatg	ctatcaacgt	gagcctgatg	tggctcagtt	tccggaagg	240
ccaagaaccc	cagggcaagg	ctaagaggca	ctgagccctc	aacccaagcc	aggctgacct	300
ctgctttgct	ttggcatgtg	agccttgctt	aagggggcat	atctgggtcc	ctagaaggcc	360
ctagatgtgg	ggcttctaga	ttaccccttc	ctcctgccat	acccgcacat	gacaatggac	420
caaattgtgcc	acacgctcgc	tcttttttac	acccagtgcc	tctgactctg	tcccatggg	480
ctggctctcca	aagctctttc	cattgcccag	ggaggggaagg	ttctgagcaa	taaagtttct	540
tagatcaatc	aaaaaaaaaa	aaaaa				565

<210> 235

<211> 476

<212> DNA

<213> Human

<400> 235

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gtacctggag	gctcaacggc	agaagcttca	ccacaaaagc	gaaatgggca	caccacaggg	120
agaaaactgg	ttgtcctgga	tgtttgaaaa	gttggtcgtt	gtcatgggtg	gttacttcat	180

cctatctatc	attaactcca	tggcacaaaag	ttatgccaaa	cgaatccagc	agcgggtgaa	240
ctcagaggag	aaaactaaat	aagtagagaa	agttttaaac	tgcagaaatt	ggagtggatg	300
ggttctgcct	taaattggga	ggactccaag	ccgggaagga	aaattccctt	ttccaacctg	360
tatcaatttt	tacaactttt	ttcctgaaag	cagtttagtc	catactttgc	actgacatac	420
tttttccttc	tgtgctaagg	taaggatatcc	accctcgatg	caatccacct	tgtttt	476

<210> 236

<211> 607

<212> DNA

<213> Human

<400> 236

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cccgcgcgagc	gaatgtaacc	cggccttgga	cgacccgacg	cggactacat	gaacctgctg	120
ggcatgatct	tcagcatgtg	cggcctcatg	cttaagctga	agtgggtgtg	ttgggtcgct	180
gtctactgct	ccttcacag	ctttgccaac	tctcggagct	cggaggacac	gaagcaaatg	240
atgagtagct	tcagtctgtc	catctctgcc	gtgggtgatgt	cctatctgca	gaatcctcag	300
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cactaggcct	gggctttggc	tgctaaacct	gctgccttca	gctgccatcc	tggacttccc	420
tgaatgaggc	cgtctcgggtg	ccccagctg	gatagagggga	acctggccct	ttcctagggga	480
acaccctagg	cttacccttc	ctgcctccct	tccctgcct	gctgctgggg	gagatgctgt	540
ccatgtttct	aggggtattc	atttgcttcc	tcgttgaaac	ctgttggttaa	taaagttttt	600
cactctg						607

<210> 237

<211> 513

<212> DNA

<213> Mouse

<400> 237

ttctccatta	cctctatgcc	taatattcat	cagccttcat	tactctctag	catattcacc	60
ttgattcaac	agattcaaac	ttcctacagc	cttctactga	tgtcttacia	gctcttgcc	120
ctgtgccttt	ctcatgctat	tctttttgct	tagattgctc	tttggtccca	gctcatgttc	180
atcactccct	tcaaagcctt	tcttccttta	tatcttctga	ctgagctctc	cctgattgac	240
atcacctcat	gcgatgacct	ccctcattct	gtgctgcctc	agcacttate	ttttgagttt	300
gtactgtgggt	ccatgtactt	actaatatgt	tgctttgtaa	ttattttcta	gcactctgtg	360
ttacagtttc	atatttgtat	ttatttccaa	aattaaattg	taagctcctt	gagggcagga	420
ataataactt	ttacatttgt	atctctgcac	ccccagtgct	ctagtatagt	gctgagcaca	480
tagtaggcgt	ttaataaatg	cttggtgaag	tat			513

<210> 238

<211> 944

<212> DNA

<213> Rat

<400> 238

ggcacgaggg	gccgcccaggt	cccgcggggt	cgggtgtagct	cgtgcgcgac	gctgcgacgc	60
tcgtgggtgc	cgtgttcggc	ttttcctgtc	tacttcagtg	caccgctgca	gctccggcct	120
cgggtctgac	gcgccacagc	atggcttccg	ctttggagga	gttgccagaaa	gacctagaag	180
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aaaaatccaa	gattgagacg	gaactaagga	acaagatgca	gcagaagtca	cagaagaaac	300
cagaatttga	taatgaaaag	ccagctgctg	tggttgctcc	tcttacaaca	gggtacactg	360
tgaaaatcag	taattatgga	tgggatcagt	cagataagtt	tgtgaaaatc	tacattactt	420
taactggagt	tcattcaggtt	cctgctgaga	atgtgcaagt	acacttcaca	gagagggtcat	480
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cgtgggtgga	atcccagagag	aagcaagcca	gggaagacac	agaattctga	ggcttttaaaa	840
gtcctgtggg	aaccgtcatg	tggagtgtct	gtgtttccag	tagggactgt	tggtgaactg	900

cacacatgtg ttcacgtggg tatgtagttt tggacagatg acta

944

<210> 239

<211> 386

<212> DNA

<213> Rat

<400> 239

ctcgtgccga	attcggcacg	agtggcgaga	tgggggaatgc	ggccctggga	gcggagctgg	60
gcgtgcgggt	cctgctcttt	gtggccttcc	tggcgaccga	gctgctccct	cccttccagc	120
ggcggattca	gcccagaggag	ctgtggcttt	accggaaccc	gtacgtggag	gcggaatact	180
tccccaccgg	ccccatgttt	gtcattgcct	ttctcaccct	actgtccctg	atcttcttctg	240
ccaagtttct	gaggaaagct	gacgccaccg	acagcaagca	agcctgcctc	gctgccagcc	300
ttgccctagc	tctgaatggg	gtctttacca	acatcataaa	actgatagtg	ggcaggccac	360
gcccgatttt	cttctaccga	tgcttc				386

<210> 240

<211> 228

<212> DNA

<213> Rat

<400> 240

ttccgcgggc	gtcatgacgg	ctgcgggtgtt	ctttgggtgc	gccttcatcg	ccttcggggcc	60
cgcgctctcc	ctttacgtct	tcaccatcgc	cactgatcct	ttgcgagtc	tcttcctcat	120
cgcgggtgcc	ttcttctggg	tggtgtctct	gctgcttctg	tctgttttct	ggttccctagt	180
gagagtcctc	actgacaaca	gagatggacc	agtacagaat	tacctgct		228

<210> 241

<211> 452

<212> DNA

<213> Human

<400> 241

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ttgttaggaa	aatgtaggct	accagtagaa	aatgacattc	tctattaata	agatctgagg	120
tgcgacacac	ataattgtcc	caatttttaa	gattgatggg	gagcatgaag	cattttttta	180
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tctgagtgag	ctaactgaca	caatgaaact	gtcaggcatg	tttctgctcc	tctctctggc	360
tcttttctgc	tttttaacag	gtgtcttcag	tcaggaggga	cagggttgact	gtggtgagtc	420
caggacacca	aggcctactg	cactcgggaa	cc			452

<210> 242

<211> 1311

<212> DNA

<213> Mouse

<400> 242

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tttttccac	ctgctgccct	cacctgagcc	cagcccagag	ggcagctacg	tgggccagca	180
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caggtcatta	ccatccccag	gctggatcac	tggagcaggc	ctcctctctg	tccatgtgag	1260
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<210> 243
 <211> 399
 <212> DNA
 <213> Mouse

<400> 243						
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ctctccaaca	tctcgtccat	caccgacctc	ggtggctttg	acccagtgtg	gcttttcctc	180
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tattctggaa	tactctgggc	tatgttttat	gtttatttct	tttttaatcg	gttgtatttt	360
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<210> 244
 <211> 1421
 <212> DNA
 <213> Mouse

<220>
 <221> unsure
 <222> (1370) ... (1370)

<221> unsure
 <222> (1395) ... (1395)

<400> 244						
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gtccttttcc	cagagctggg	tctgtgggtc	aacatgggtc	cctgcttctc	cctgtctctg	180
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<210> 245
 <211> 461
 <212> DNA
 <213> Mouse

<400> 245
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 gctagcccca aactcagaaa tctgcctccc gagtgctggg actaaggggtg tgcaccacca 180
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 ggcagccgtg gtccgtgtctg aatattgtct ctaactgcca cagtttcaga gaaaggggaa 420
 caagttctcc tttgcttctt gccctccag atagaccctt g 461

<210> 246
 <211> 1280
 <212> DNA
 <213> Mouse

<400> 246
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<210> 247
 <211> 833
 <212> DNA
 <213> Rat

<400> 247
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<213> Human

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<211> 1464

<212> DNA

<213> Mouse

<400> 255

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<210> 258

<211> 946

<212> DNA

<213> Mouse

<400> 258

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<210> 259

<211> 1018

<212> DNA

<213> Human

<400> 259

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<210> 260

<211> 2800

<212> DNA

<213> Mouse

<400> 260

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<210> 261

<211> 1335

<212> DNA

<213> Mouse

<400> 261

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<210> 262
 <211> 1816
 <212> DNA
 <213> Mouse

<400> 262

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<210> 263
 <211> 764
 <212> DNA
 <213> Mouse

<400> 263

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<210> 264
 <211> 1697
 <212> DNA

<213> Mouse

<400> 264

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tttggagctg	ctgtcttcac	tatcatcatg	actctacgcc	aggctattgc	catcctcctc	1200
tcctgcctcc	tctatggcca	tactgtcact	gtgggtggggg	gactgggagt	agctgtggtc	1260
ttcactgccc	tcctactcag	agtctatgcc	cggggccgga	agcagcgggg	aaagaaggct	1320
gtgcccactg	agcccccagt	acagaagggtg	tgagcagtg	agtaaagacc	ctcatcttct	1380
gaggcactgg	ctcagtatca	gcatacagca	gaggattgga	gccctggagg	cagcctcttt	1440
tgccttaaaa	gccccactt	catggaaatg	acagctgtgg	gtgttttggt	agaggtgacc	1500
cagagctcct	cccccaatct	ctgaaatctt	gctgggtggcc	aagcaaacca	gcaccagggc	1560
tttgcata	gcacgcaccc	ttgaggctac	caggcaccag	ctgggaagag	aatttacagg	1620
tcctgcagtt	cccctagggg	ccagtgaaga	tggtgctgtg	ccagaaggga	caaaggcccc	1680
cagcccagtt	ggggccc					1697

<210> 265

<211> 159

<212> DNA

<213> Mouse

<220>

<400> 265

gttttcttct	ccaggctgaa	gacctgaacg	tcaagttgga	aggggagcct	tccatgcgga	60
aaccaaagca	gcggccgcgg	cggagcccc	tcateatccc	caccaaggcg	ggcactttca	120
tcgcccctcc	tgtctactcc	aacatcacc	cttaccaga			159

<210> 266

<211> 292

<212> DNA

<213> Mouse

<400> 266

gtgggggtccc	agacttgcca	accaaagggc	cattcctggt	atatggttct	ggettcagct	60
ctgggtggcat	ggactatggt	atggttggtg	gcaaggaggc	tgggaccgag	tctcgcttca	120
aacagtggac	ctcaatgatg	gaagggtgc	catctgtggc	cacacaagaa	gccaccatgc	180
acaaaaacgg	cgctatagtg	gcccctggta	agacccgagg	aggttcacca	tacaaccagt	240
ttgatataat	cccaggtgac	acactgggtg	gccatacggg	tcctgctggt	ga	292

<210> 267

<211> 339

<212> DNA

<213> Mouse

<400> 267

ccactgacct	tcccagaagg	tgacagccgg	cggcggatgt	tgtcaaggag	ccgagatagt	60
ccagcagtgc	ctcggtagcc	agaagacggg	ctgtctcccc	ccaaaagacg	gcgacattcg	120
atgagaagtc	accacagtga	tctcacattt	tgcgagatta	tctgatgga	gatggagtcc	180
catgatgcag	cctggccttt	cctagagcct	gtgaaccctc	gcttggtgag	tggataccga	240
cgtgtcatca	agaaccctat	ggatttttcc	accatgcgag	aacgcctgct	ccgtggaggg	300
tacactagct	cagaagagtt	tgacagctgat	gctctgctg			339

<210> 268

<211> 153

<212> DNA

<213> Mouse

<400> 268

ctgaagttct	ctcattcctt	tctggaagac	cataatagtt	actgcattaa	tggagcatgt	60
gcattccacc	atgagctgaa	gcaagccatt	tgacagatgct	ttactgggta	tacgggacaa	120
cgatgtgagc	atttgaccct	aacttcgtat	gct			153

<210> 269

<211> 153

<212> DNA

<213> Human

<400> 269

ttgaagttct	cacacctttg	cctggaagat	cataacagtt	actgcatcaa	cggtgcttgt	60
gcattccacc	atgagctaga	gaaagccatc	tgacaggtgt	ttactgggta	tactggagaa	120
aggtgtgagc	acttgacttt	aacttcatat	gct			153

<210> 270

<211> 288

<212> DNA

<213> Human

<400> 270

gcggccgcgc	tgctcctgct	gctgctggcg	ctgtacaccg	cgcggtgtgga	cggttcctaaa	60
tgcaagtgtc	cccgggaagg	acccaagatc	cgctacagcg	acgtgaagaa	gctggaaatg	120
aagccaaagt	accgcactg	cgaggagaag	atggttatca	tcaccaccaa	gagcgtgtcc	180
aggtaccgag	gtcaggagca	ctgcctgcac	cccaagctgc	agagcaccaa	gcgcttcac	240
aagtgggtaca	acgcctggaa	cgagaagcgc	agggtctacg	aagaatag		288

<210> 271

<211> 234

<212> DNA

<213> Mouse

<400> 271

tccaagtgtg	agtgttcccc	gaagggggccc	aagatccgct	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtaccc	acactgagag	gagaagatgg	ttatcgtcac	caccaagagc	120
atgtccaggt	accggggcca	ggagcactgc	ctgcacccta	agctgcagag	caccaaaccg	180
ttcatcaagt	ggtacaatgc	ctggaacgag	aagcgcaggg	tctacgaaga	atag	234

<210> 272

<211> 234

<212> DNA

<213> Human

<400> 272

tccaaatgca	agtgttcccc	gaaggggaccc	aagatccgct	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtaccc	gcactgagag	gagaagatgg	ttatcatcac	caccaagagc	120
gtgtccaggt	accgaggtca	ggagcactgc	ctgcacccca	agctgcagag	caccaagcgc	180

ttcatcaagt ggtacaacgc ctggaacgag aagcgcaggg tctacgaaga atag

234

<210> 273
 <211> 645
 <212> DNA
 <213> Mouse

<400> 273

atgctgtcgc	tccgctcctt	gcttccacac	ctgggactgt	tcctgtgcct	ggctctgcac	60
ttatccccct	ccctctctgc	cagtataat	gggtcctgcg	tggtccttga	taacatctac	120
acctccgaca	tcttggaat	cagcactatg	gctaactgtt	ctgggtggga	tgtaacctat	180
acagtgcgg	tccccgtgaa	cgattcagtc	agtgccgtga	tcctgaaagc	agtgaaggag	240
gacgacagcc	cagtgggcac	ctggagtggg	acatatgaga	agtgcacga	cagcagtgtc	300
tactataact	tgacatccca	aagccagtcg	gtcttccaga	caaactggac	agttcctact	360
tccgaggatg	tgactaaagt	caacctgcag	gtcctcatcg	tcgtcaatcg	cacagcctca	420
aagtcacccg	tgaaaatgga	acaagtacaa	ccctcagcct	caacccttat	tcctgagagt	480
tctgagacca	gccagaccat	aaacacgact	ccaactgtga	acacagccaa	gactacagcc	540
aaggacacag	ccaacaccac	agccgtgacc	acagccaata	ccacagccaa	taccacagcc	600
gtgaccacag	ccaagaccac	agccaaaagc	ctggccatcc	gcact		645

<210> 274
 <211> 63
 <212> DNA
 <213> Mouse

<400> 274

gggtacagtg	atggttacca	agtgtgtagt	aggttcggaa	gcaaagtgcc	tcagtttctg	60
aac						63

<210> 275
 <211> 388
 <212> PRT
 <213> Mouse
 <400> 275

Met	Gly	Leu	Glu	Pro	Ser	Trp	Tyr	Leu	Leu	Leu	Cys	Leu	Ala	Val	Ser
1				5				10						15	
Gly	Ala	Ala	Gly	Thr	Asp	Pro	Pro	Thr	Ala	Pro	Thr	Thr	Ala	Glu	Arg
			20					25					30		
Gln	Arg	Gln	Pro	Thr	Asp	Ile	Ile	Leu	Asp	Cys	Phe	Leu	Val	Thr	Glu
		35				40						45			
Asp	Arg	His	Arg	Gly	Ala	Phe	Ala	Ser	Ser	Gly	Asp	Arg	Glu	Arg	Ala
	50					55					60				
Leu	Leu	Val	Leu	Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu
65				70						75				80	
Gly	Ile	Thr	Asp	Phe	Gln	Gly	Ser	Thr	Glu	Thr	Lys	Gln	Asp	Ser	Pro
			85					90					95		
Val	Ile	Phe	Glu	Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu
			100					105					110		
Ala	Leu	Leu	His	Ala	Asp	Cys	Ser	Gly	Lys	Ala	Val	Thr	Cys	Glu	Ile
		115					120					125			
Ser	Lys	Tyr	Phe	Leu	Gln	Ala	Arg	Gln	Glu	Ala	Thr	Phe	Glu	Lys	Ala
	130					135					140				
His	Trp	Phe	Ile	Ser	Asn	Met	Gln	Val	Ser	Arg	Gly	Gly	Pro	Ser	Val
145				150					155					160	
Ser	Met	Val	Met	Lys	Thr	Leu	Arg	Asp	Ala	Glu	Val	Gly	Ala	Val	Arg
			165					170					175		
His	Pro	Thr	Leu	Asn	Leu	Pro	Leu	Ser	Ala	Gln	Gly	Thr	Val	Lys	Thr
		180					185					190			
Gln	Val	Glu	Phe	Gln	Val	Thr	Ser	Glu	Thr	Gln	Thr	Leu	Asn	His	Leu
	195					200					205				
Leu	Gly	Ser	Ser	Val	Ser	Leu	His	Cys	Ser	Phe	Ser	Met	Ala	Pro	Asp

210 215 220
 Leu Asp Leu Thr Gly Val Glu Trp Arg Leu Gln His Lys Gly Ser Gly
 225 230 235 240
 Gln Leu Val Tyr Ser Trp Lys Thr Gly Gln Gly Gln Ala Lys Arg Lys
 245 250 255
 Gly Ala Thr Leu Glu Pro Glu Glu Leu Leu Arg Ala Gly Asn Ala Ser
 260 265 270
 Leu Thr Leu Pro Asn Leu Thr Leu Lys Asp Glu Gly Thr Tyr Ile Cys
 275 280 285
 Gln Ile Ser Thr Ser Leu Tyr Gln Ala Gln Gln Ile Met Pro Leu Asn
 290 295 300
 Ile Leu Ala Pro Pro Lys Val Gln Leu His Leu Ala Asn Lys Asp Pro
 305 310 315 320
 Leu Pro Ser Leu Val Cys Ser Ile Ala Gly Tyr Tyr Pro Leu Asp Val
 325 330 335
 Gly Val Thr Trp Ile Arg Glu Glu Leu Gly Gly Ile Pro Ala Gln Val
 340 345 350
 Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Thr Met Gly Thr Tyr
 355 360 365
 Ser Ile Ser Ser Thr Val Met Ala Asp Pro Gly Pro Thr Gly Ala Thr
 370 375 380
 Tyr Thr Cys Gln
 385

<210> 276

<211> 151

<212> PRT

<213> Rat

<400> 276

Met Ala Glu Pro Trp Ala Gly Gln Phe Leu Gln Ala Leu Pro Ala Thr
 1 5 10 15
 Val Leu Gly Ala Leu Gly Thr Leu Gly Ser Glu Phe Leu Arg Glu Trp
 20 25 30
 Glu Thr Gln Asp Met Arg Val Thr Leu Phe Lys Leu Leu Leu Trp
 35 40 45
 Leu Val Leu Ser Leu Leu Gly Ile Gln Leu Ala Trp Gly Phe Tyr Gly
 50 55 60
 Asn Thr Val Thr Gly Leu Tyr His Arg Pro Gly Lys Trp Gln Gln Met
 65 70 75 80
 Lys Leu Ser Lys Leu Thr Glu Asn Lys Gly Arg Gln Gln Glu Lys Gly
 85 90 95
 Leu Gln Arg Tyr Arg Trp Val Cys Trp Leu Leu Cys Cys Thr Leu Leu
 100 105 110
 Leu Ser Arg Pro Leu Arg Gln Leu Gln Arg Ala Trp Val Gly Gly Leu
 115 120 125
 Glu Tyr His Asp Ala Pro Arg Val Ser Leu His Cys Pro Gln Pro Cys
 130 135 140
 Leu Gln Gln Arg Gln Val Leu
 145 150

<210> 277

<211> 163

<212> PRT

<213> Rat

<400> 277

Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr
 1 5 10 15
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe
 20 25 30

Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala
 35 40 45
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn
 50 55 60
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val
 65 70 75 80
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu
 85 90 95
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr
 100 105 110
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys
 115 120 125
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser
 130 135 140
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg
 145 150 155 160
 Trp Lys Asn

<210> 278

<211> 330

<212> PRT

<213> Rat

<400> 278

Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1 5 10 15
 Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
 20 25 30
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35 40 45
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50 55 60
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65 70 75 80
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85 90 95
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
 100 105 110
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
 115 120 125
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
 130 135 140
 Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
 145 150 155 160
 Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
 165 170 175
 Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
 180 185 190
 Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
 195 200 205
 Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
 210 215 220
 Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
 225 230 235 240
 Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
 245 250 255
 Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
 260 265 270
 Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
 275 280 285

Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
 290 295 300
 Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
 305 310 315 320
 His Arg Lys Ala Phe Leu Pro Phe Leu Phe
 325 330

<210> 279
 <211> 61
 <212> PRT
 <213> Rat

<400> 279
 Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
 1 5 10 15
 His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
 20 25 30
 Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
 35 40 45
 Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
 50 55 60

<210> 280
 <211> 105
 <212> PRT
 <213> Rat

<400> 280
 Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
 1 5 10 15
 Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
 20 25 30
 Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
 35 40 45
 Phe Arg Gly Tyr Gln Gly Pro Gly Pro Pro Gly Pro Pro Gly Ile
 50 55 60
 Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
 65 70 75 80
 Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
 85 90 95
 Glu Arg Gly Gln His Gly Pro Lys Gly
 100 105

<210> 281
 <211> 27
 <212> PRT
 <213> Mouse

<400> 281
 Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
 1 5 10 15
 Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
 20 25

<210> 282
 <211> 169
 <212> PRT
 <213> Mouse

<400> 282
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly

```

1      5      10      15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
      20      25      30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
      35      40      45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
      50      55      60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
65      70      75      80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
      85      90      95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
      100      105      110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
      115      120      125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
      130      135      140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145      150      155      160
Gly Glu Met Pro Pro Glu Asp Gly Met
      165

```

<210> 283
 <211> 61
 <212> PRT
 <213> Mouse

```

      <400> 283
Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
1      5      10      15
Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
      20      25      30
Thr Val Thr Gln Met Arg Thr Ile Ile Ile Thr Met Asp Gln Leu Arg
      35      40      45
Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
50      55      60

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<210> 284
 <211> 131
 <212> PRT
 <213> Mouse

```

      <400> 284
Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
1      5      10      15
Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
      20      25      30
Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
      35      40      45
Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
50      55      60
Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
65      70      75      80
Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
      85      90      95
Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
      100      105      110
Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
      115      120      125
Leu Arg Arg
130

```

<210> 285
 <211> 78
 <212> PRT
 <213> Mouse

<400> 285
 Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
 1 5 10 15
 Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
 20 25 30
 Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
 35 40 45
 Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
 50 55 60
 Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
 65 70 75

<210> 286
 <211> 206
 <212> PRT
 <213> Mouse

<400> 286
 Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
 1 5 10 15
 Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
 20 25 30
 Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
 35 40 45
 Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
 50 55 60
 Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
 65 70 75 80
 Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
 85 90 95
 Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
 100 105 110
 Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser
 115 120 125
 Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
 130 135 140
 Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
 145 150 155 160
 Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
 165 170 175
 His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
 180 185 190
 Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser
 195 200 205

<210> 287
 <211> 169
 <212> PRT
 <213> Mouse

<400> 287
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20 25 30

Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35 40 45
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50 55 60
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65 70 75 80
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85 90 95
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
 100 105 110
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
 115 120 125
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
 130 135 140
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
 145 150 155 160
 Gly Glu Met Pro Pro Glu Asp Gly Met
 165

<210> 288
 <211> 114
 <212> PRT
 <213> Mouse

<400> 288
 Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
 1 5 10 15
 Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
 20 25 30
 Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
 35 40 45
 Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
 50 55 60
 His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
 65 70 75 80
 Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
 85 90 95
 Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
 100 105 110
 Ser Leu

<210> 289
 <211> 46
 <212> PRT
 <213> Mouse

<400> 289
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
 1 5 10 15
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
 20 25 30
 Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
 35 40 45

<210> 290
 <211> 199
 <212> PRT
 <213> Mouse

<400> 290

Met Val Leu Pro Thr Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
 1 5 10 15
 Leu Gly Gly Glu Thr Arg Pro Arg Ala Ala Thr Glu Arg Arg Ser Val
 20 25 30
 Gly Pro Ser Ala Arg Arg Gly Ala Gly Pro Arg Val Ser Gly Leu Leu
 35 40 45
 Gly Phe Cys Gln Leu Ser Gln Leu Ala Ser Ala Asp Pro Glu Arg Arg
 50 55 60
 Ser Pro Arg Ala Ile Val Pro Arg Ala Pro Arg Pro Arg Ser Arg Arg
 65 70 75 80
 Arg Pro Cys Leu Pro Gly Phe Ser Arg Arg Phe Pro Arg Glu Arg Arg
 85 90 95
 Ser Pro Gly Gln Pro Pro Ser Arg Thr Pro Gln Pro Pro Gln Pro Cys
 100 105 110
 Arg Gly Pro Ser Pro Gly Thr Ala Gln Thr Arg Ser Asn Leu Arg Gly
 115 120 125
 Trp Gln Arg Gly Gly Ser Ile Val Leu Gln Ala Ser Glu Arg Thr Arg
 130 135 140
 Ala Gly Cys Arg Thr Pro Val Cys Val Ser His Pro Ser Ala Phe Pro
 145 150 155 160
 Pro Pro Arg Ala Leu Phe Gly Val Phe Val Ala Ser Ala Pro Glu Val
 165 170 175
 Val Cys Val Cys Val Ser Val Val Leu Ser Val Cys Leu Leu Ser Pro
 180 185 190
 Arg Gly Lys Thr Leu Val Asp
 195

<210> 291

<211> 568

<212> PRT

<213> Rat

<400> 291

Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1 5 10 15
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
 20 25 30
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
 35 40 45
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
 50 55 60
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
 65 70 75 80
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
 85 90 95
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
 100 105 110
 Gln Lys Gln Gln Met Thr Asp Val Glu Gly Thr Glu Leu Phe Ser Tyr
 115 120 125
 Lys Gly Asn Asp Val Glu Tyr Phe Leu Ser Ser Ser Pro Ser Gly
 130 135 140
 Leu Tyr Gln Leu Glu Leu Leu Ser Thr Glu Lys Asp Thr His Phe Lys
 145 150 155 160
 Val Tyr Ala Thr Thr Thr Pro Glu Ser Asp Gln Pro Tyr Pro Asp Leu
 165 170 175
 Pro Tyr Asp Pro Arg Val Asp Val Thr Ser Ile Gly Arg Thr Thr Val
 180 185 190
 Thr Leu Ala Trp Lys Gln Ser Pro Thr Ala Ser Met Leu Lys Gln Pro
 195 200 205
 Ile Glu Tyr Cys Val Val Ile Asn Lys Glu His Asn Phe Lys Ser Leu
 210 215 220

Cys Ala Ala Glu Thr Lys Met Ser Ala Asp Asp Ala Phe Met Val Ala
 225 230 235 240
 Pro Lys Pro Gly Leu Asp Phe Ser Pro Phe Asp Phe Ala His Phe Gly
 245 250 255
 Phe Pro Thr Asp Asn Leu Gly Lys Asp Arg Ser Phe Leu Ala Lys Pro
 260 265 270
 Ser Pro Lys Val Gly Arg His Val Tyr Trp Arg Pro Lys Val Asp Ile
 275 280 285
 Lys Lys Ile Cys Ile Gly Ser Lys Asn Ile Phe Thr Val Ser Asp Leu
 290 295 300
 Lys Pro Asn Thr Gln Tyr Tyr Phe Asp Val Phe Met Val Asn Thr Asn
 305 310 315 320
 Thr Asn Met Asn Thr Ala Phe Val Gly Ala Phe Ala Arg Thr Lys Glu
 325 330 335
 Glu Ala Lys Gln Lys Thr Val Glu Leu Lys Asp Gly Arg Val Thr Asp
 340 345 350
 Val Val Val Lys Arg Lys Gly Lys Lys Phe Leu Arg Phe Ala Pro Val
 355 360 365
 Ser Ser His Gln Lys Val Thr Leu Phe Ile His Ser Cys Met Asp Thr
 370 375 380
 Val Gln Val Gln Val Arg Arg Asp Gly Lys Leu Leu Leu Ser Gln Asn
 385 390 395 400
 Val Glu Gly Ile Arg Gln Phe Gln Leu Arg Gly Lys Pro Lys Gly Lys
 405 410 415
 Tyr Leu Ile Arg Leu Lys Gly Asn Lys Lys Gly Ala Ser Met Leu Lys
 420 425 430
 Ile Leu Ala Thr Thr Arg Pro Ser Lys His Ala Phe Pro Ser Leu Pro
 435 440 445
 Asp Asp Thr Arg Ile Lys Ala Phe Asp Lys Leu Arg Thr Cys Ser Ser
 450 455 460
 Val Thr Val Ala Trp Leu Gly Thr Gln Glu Arg Arg Lys Phe Cys Ile
 465 470 475 480
 Tyr Arg Lys Glu Val Gly Gly Asn Tyr Ser Glu Glu Gln Lys Arg Arg
 485 490 495
 Glu Arg Asn Gln Cys Leu Gly Pro Asp Thr Arg Lys Lys Ser Glu Lys
 500 505 510
 Val Leu Cys Lys Tyr Phe His Ser Gln Asn Leu Gln Lys Ala Val Thr
 515 520 525
 Thr Glu Thr Ile Arg Asp Leu Gln Pro Gly Lys Ser Tyr Leu Leu Asp
 530 535 540
 Val Tyr Val Val Gly His Gly Gly His Ser Val Lys Tyr Gln Ser Lys
 545 550 555 560
 Leu Val Lys Thr Arg Lys Val Cys
 565

<210> 292

<211> 123

<212> PRT

<213> Mouse

<400> 292

Met Leu Thr Glu Pro Ala Gln Leu Phe Val His Lys Lys Asn Gln Pro
 1 5 10 15
 Pro Ser His Ser Ser Leu Arg Leu His Phe Arg Thr Leu Ala Gly Ala
 20 25 30
 Leu Ala Leu Ser Ser Thr Gln Met Ser Trp Gly Leu Gln Ile Leu Pro
 35 40 45
 Cys Leu Ser Leu Ile Leu Leu Leu Trp Asn Gln Val Pro Gly Leu Glu
 50 55 60
 Gly Gln Glu Phe Arg Phe Gly Ser Cys Gln Val Thr Gly Val Val Leu
 65 70 75 80

Pro Glu Leu Trp Glu Ala Phe Trp Thr Val Lys Asn Thr Val Gln Thr
 85 90 95
 Gln Asp Asp Ile Thr Ser Ile Arg Leu Leu Lys Pro Gln Val Leu Arg
 100 105 110
 Asn Val Ser Val Ile Arg Trp Glu Gly Asp Ser
 115 120

<210> 293
 <211> 66
 <212> PRT
 <213> Mouse

<400> 293
 Met Asp Val Trp Ser Gly Leu Pro Leu Glu Thr Leu Trp Ile Tyr Glu
 1 5 10 15
 Ala Val Leu Pro Trp Leu Leu Met Gly Gln Gly His Ala Trp Val Cys
 20 25 30
 Gly Pro Ile Ala Leu Trp Val Phe Val Asn Val Pro Gly Leu Cys Tyr
 35 40 45
 His Gln Lys Pro Phe Arg Cys Pro Trp Ser Gly Leu Leu Pro Glu Ala
 50 55 60
 Leu Cys
 65

<210> 294
 <211> 294
 <212> PRT
 <213> Rat

<400> 294
 Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
 1 5 10 15
 Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
 20 25 30
 Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
 35 40 45
 Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly
 50 55 60
 Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
 65 70 75 80
 Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
 85 90 95
 Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
 100 105 110
 Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
 115 120 125
 His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro
 130 135 140
 Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
 145 150 155 160
 Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
 165 170 175
 Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
 180 185 190
 Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Tyr Tyr Phe Thr Tyr
 195 200 205
 Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile Gly Leu Val His Asn
 210 215 220
 Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn His Asp
 225 230 235 240
 Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp Glu Val

245 250 255
 Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro
 260 265 270
 Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln
 275 280 285
 Gly Asp Pro Asn Glu Val
 290

<210> 295

<211> 243

<212> PRT

<213> Rat

<400> 295

Met Arg Pro Leu Leu Ala Leu Leu Leu Leu Gly Leu Ala Ser Gly Ser
 1 5 10 15
 Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly Gln Pro
 20 25 30
 Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly Leu Pro Gly
 35 40 45
 Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu
 50 55 60
 Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Glu Pro
 65 70 75 80
 Gly Pro Arg Gly Glu Ala Gly Pro Val Gly Ala Ile Gly Pro Ala Gly
 85 90 95
 Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu
 100 105 110
 Ser Arg Val Pro Pro Pro Ala Asp Thr Pro Leu Pro Phe Asp Arg Val
 115 120 125
 Leu Leu Asn Glu Gln Gly His Tyr Asp Ala Thr Thr Gly Lys Phe Thr
 130 135 140
 Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr
 145 150 155 160
 Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala
 165 170 175
 Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser
 180 185 190
 Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln
 195 200 205
 Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp
 210 215 220
 Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro
 225 230 235 240
 Val Phe Ala

<210> 296

<211> 444

<212> PRT

<213> Rat

<400> 296

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1 5 10 15
 Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
 20 25 30
 Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
 35 40 45
 Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
 50 55 60

Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
 65 70 75 80
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
 85 90 95
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
 100 105 110
 Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
 115 120 125
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
 130 135 140
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
 145 150 155 160
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
 165 170 175
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
 180 185 190
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
 195 200 205
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
 210 215 220
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
 225 230 235 240
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
 245 250 255
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
 260 265 270
 Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp
 275 280 285
 Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser
 290 295 300
 Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys
 305 310 315 320
 His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe
 325 330 335
 Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe
 340 345 350
 Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val
 355 360 365
 Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val
 370 375 380
 Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys
 385 390 395 400
 Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys
 405 410 415
 Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys
 420 425 430
 Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys
 435 440

<210> 297

<211> 65

<212> PRT

<213> Human

<400> 297

Met Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser
 1 5 10 15
 Arg Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser
 20 25 30
 Trp Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala
 35 40 45

Leu Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser
 50 55 60
 Leu
 65

<210> 298
 <211> 52
 <212> PRT
 <213> Human

<400> 298
 Met Lys Ile Asn Ile Ile Gln Gly Ser Ile Met Ile Leu Leu Ile Cys
 1 5 10 15
 Leu Ser Gln Thr Cys Thr Ser Leu Pro Val Gln Glu Ala Leu Ile Thr
 20 25 30
 Phe Cys His Leu Tyr Phe Thr Tyr Cys Tyr Ser Gly Asn Ser Asn Lys
 35 40 45
 Met Gln Val Leu
 50

<210> 299
 <211> 41
 <212> PRT
 <213> Human

<400> 299
 Met Pro Cys Val Leu Phe Phe Phe Phe Phe Leu Ser Thr Ser Lys Ser
 1 5 10 15
 Met Ile Tyr Ser Ser Leu Met Leu Gly Leu Tyr Ile Pro Ser Glu Ala
 20 25 30
 Cys Val Leu Gly Leu Lys Phe Lys Phe
 35 40

<210> 300
 <211> 80
 <212> PRT
 <213> Mouse

<400> 300
 Met Val Trp Gly Thr Leu Leu Gly Arg Val Leu Ala Ala Leu Leu Asn
 1 5 10 15
 Ile Val Pro Thr Glu Ser Ser Tyr Arg Ser Pro Ser Phe Leu Ala Gly
 20 25 30
 Phe Arg Phe Cys Cys Ser Pro Trp Ser Gln His Phe Gly Cys Gly Arg
 35 40 45
 Leu Thr Ser Cys Leu Pro Pro Cys Val Asp Arg Val Val Lys Thr Tyr
 50 55 60
 Ser Ser Pro Pro Cys Leu Ser Val Asn Gly His Asp Val Thr Ile Cys
 65 70 75 80

<210> 301
 <211> 82
 <212> PRT
 <213> Mouse

<400> 301
 Met Gly Ser Val Leu Thr Ser Cys Phe Cys Val Gly Gly Ser Ala Glu
 1 5 10 15
 Ala Trp Asn Trp Leu Pro Ser Ala Ser Ser Leu Phe Pro Cys Cys Ile
 20 25 30
 Ala Thr Leu Leu Pro Leu Leu Phe Leu Leu Pro His Leu His Ser Thr

35	40	45
Leu Ser Arg Val Gln Arg	Leu Asn Phe Asn Ile	Gly His Leu Gly Val
50	55	60
Tyr Leu Tyr Val Asn Asn	Asp Ile Arg Ser Arg	Val Thr Pro Leu Leu
65	70	75
Ser Ser		80

<210> 302

<211> 411

<212> PRT

<213> Rat

<400> 302

Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val	1	5	10	15
Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala	20	25	30	
Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val	35	40	45	
Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val	50	55	60	
Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe	65	70	75	80
Ala Gly Glu Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr	85	90	95	
Asp Val Ala Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val	100	105	110	
Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Ile Thr Gly	115	120	125	
Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Lys Lys His Ala	130	135	140	
Lys Gly Val Arg Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr	145	150	155	160
Asp Asp Phe Arg Ser Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu	165	170	175	
Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe	180	185	190	
Val Val Glu Val Trp Ser Gln Leu Leu Ser Gln Lys His Val Gly Leu	195	200	205	
Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu	210	215	220	
Leu Val Ile Leu Val Ile Pro Pro Ala Val Thr Pro Gly Thr Asp Gln	225	230	235	240
Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Ile Leu	245	250	255	
Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ser Gln Gln Pro	260	265	270	
Gly Pro Asn Ala Pro Leu Ser Trp Ile Arg Ala Cys Val Gln Val Leu	275	280	285	
Asp Pro Lys Ser Gln Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe	290	295	300	
Tyr Gly Met Asp Tyr Ala Ala Ser Lys Asp Ala Arg Glu Pro Val Ile	305	310	315	320
Gly Ala Arg Ala Val Leu Lys Val Ala Leu Pro Leu Ala Val Ser Ser	325	330	335	
Gln Gln Ile Trp Thr Leu Gly Arg Gly Gly Ser Thr Ser Ala Leu Leu	340	345	350	
Leu Ala Gly Leu Gly Leu Ala Ser Glu Pro Cys Thr Lys Ser Glu Glu	355	360	365	
Val Pro Lys Lys Ser Leu Leu Asp Thr Val Trp His Trp Gln Gly Glu				

370	375	380
Pro Gly Ala Leu Cys Arg Gly Arg Leu His Thr Trp Ile Leu Val Ser		
385	390	395
Ala Val Pro Gln Ala Cys Thr Cys Leu Phe Gln		400
405	410	

<210> 303
 <211> 617
 <212> PRT
 <213> Mouse

<400> 303

Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu	
1 5 10 15	
Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg	
20 25 30	
Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe	
35 40 45	
Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys	
50 55 60	
Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser	
65 70 75 80	
Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His	
85 90 95	
Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr	
100 105 110	
Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu	
115 120 125	
Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu	
130 135 140	
Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala	
145 150 155 160	
Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser	
165 170 175	
Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp	
180 185 190	
Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr	
195 200 205	
Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp	
210 215 220	
Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp	
225 230 235 240	
Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro	
245 250 255	
Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro	
260 265 270	
Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr	
275 280 285	
Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser	
290 295 300	
Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu	
305 310 315 320	
Pro Ser Trp Thr Val Ser Met Asp Thr Gln Ala Gln Gln Leu Thr Leu	
325 330 335	
His Phe Ser Ser Arg Thr Tyr Ala Thr Phe Ser Ala Ala Trp Ser Asp	
340 345 350	
Pro Gly Leu Gly Pro Asp Thr Pro Met Pro Pro Val Tyr Ser Ile Ser	
355 360 365	
Gln Thr Gln Gly Ser Val Pro Val Thr Leu Asp Leu Ile Ile Pro Phe	
370 375 380	
Leu Arg Gln Glu Asn Cys Ile Leu Val Trp Arg Ser Asp Val His Phe	

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<210> 304
<211> 72
<212> PRT
<213> Mouse
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<210> 305
<211> 649
<212> PRT
<213> Mouse
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117

Leu	Gln	Asn	Asn	Gln	Ile	Asn	Asn	Val	Gly	Ile	Pro	Ser	Asp	Leu	Lys
65					70					75					80
Asn	Leu	Leu	Lys	Val	Gln	Arg	Ile	Tyr	Leu	Tyr	His	Asn	Ser	Leu	Asp
				85					90					95	
Glu	Phe	Pro	Thr	Asn	Leu	Pro	Lys	Tyr	Val	Lys	Glu	Leu	His	Leu	Gln
				100					105					110	
Glu	Asn	Asn	Ile	Arg	Thr	Ile	Thr	Tyr	Asp	Ser	Leu	Ser	Lys	Ile	Pro
				115					120					125	
Tyr	Leu	Glu	Glu	Leu	His	Leu	Asp	Asp	Asn	Ser	Val	Ser	Ala	Val	Ser
				130					135					140	
Ile	Glu	Glu	Gly	Ala	Phe	Arg	Asp	Ser	Asn	Tyr	Leu	Arg	Leu	Leu	Phe
145					150					155					160
Leu	Ser	Arg	Asn	His	Leu	Ser	Thr	Ile	Pro	Gly	Gly	Leu	Pro	Arg	Thr
				165						170					175
Ile	Glu	Glu	Leu	Arg	Leu	Asp	Asp	Asn	Arg	Ile	Ser	Thr	Ile	Ser	Ser
				180					185					190	
Pro	Ser	Leu	His	Gly	Leu	Thr	Ser	Leu	Lys	Arg	Leu	Val	Leu	Asp	Gly
				195					200					205	
Asn	Leu	Leu	Asn	Asn	His	Gly	Leu	Gly	Asp	Lys	Val	Phe	Phe	Asn	Leu
				210					215					220	
Val	Asn	Leu	Thr	Glu	Leu	Ser	Leu	Val	Arg	Asn	Ser	Leu	Thr	Ala	Ala
225					230					235					240
Pro	Val	Asn	Leu	Pro	Gly	Thr	Ser	Leu	Arg	Lys	Leu	Tyr	Leu	Gln	Asp
				245					250					255	
Asn	His	Ile	Asn	Arg	Val	Pro	Pro	Asn	Ala	Phe	Ser	Tyr	Leu	Arg	Gln
				260					265					270	
Leu	Tyr	Arg	Leu	Asp	Met	Ser	Asn	Asn	Asn	Leu	Ser	Asn	Leu	Pro	Gln
				275					280					285	
Gly	Ile	Phe	Asp	Asp	Leu	Asp	Asn	Ile	Thr	Gln	Leu	Ile	Leu	Arg	Asn
				290					295					300	
Asn	Pro	Trp	Tyr	Cys	Gly	Cys	Lys	Met	Lys	Trp	Val	Arg	Asp	Trp	Leu
305					310					315					320
Gln	Ser	Leu	Pro	Val	Lys	Val	Asn	Val	Arg	Gly	Leu	Met	Cys	Gln	Ala
				325					330					335	
Pro	Glu	Lys	Val	Arg	Gly	Met	Ala	Ile	Lys	Asp	Leu	Ser	Ala	Glu	Leu
				340					345					350	
Phe	Asp	Cys	Lys	Asp	Ser	Gly	Ile	Val	Ser	Thr	Ile	Gln	Ile	Thr	Thr
				355					360					365	
Ala	Ile	Pro	Asn	Thr	Ala	Tyr	Pro	Ala	Gln	Gly	Gln	Trp	Pro	Ala	Pro
				370					375					380	
Val	Thr	Lys	Gln	Pro	Asp	Ile	Lys	Asn	Pro	Lys	Leu	Ile	Lys	Asp	Gln
385					390					395					400
Arg	Thr	Thr	Gly	Ser	Pro	Ser	Arg	Lys	Thr	Ile	Leu	Ile	Thr	Val	Lys
				405					410					415	
Ser	Val	Thr	Pro	Asp	Thr	Ile	His	Ile	Ser	Trp	Arg	Leu	Ala	Leu	Pro
				420					425					430	
Met	Thr	Ala	Leu	Arg	Leu	Ser	Trp	Leu	Lys	Leu	Gly	His	Ser	Pro	Ala
				435					440					445	
Phe	Gly	Ser	Ile	Thr	Glu	Thr	Ile	Val	Thr	Gly	Glu	Arg	Ser	Glu	Tyr
				450					455					460	
Leu	Val	Thr	Ala	Leu	Glu	Pro	Glu	Ser	Pro	Tyr	Arg	Val	Cys	Met	Val
465					470					475					480
Pro	Met	Glu	Thr	Ser	Asn	Leu	Tyr	Leu	Phe	Asp	Glu	Thr	Pro	Val	Cys
				485					490					495	
Ile	Glu	Thr	Gln	Thr	Ala	Pro	Leu	Arg	Met	Tyr	Asn	Pro	Thr	Thr	Thr
				500					505					510	
Leu	Asn	Arg	Glu	Gln	Glu	Lys	Glu	Pro	Tyr	Lys	Asn	Pro	Asn	Leu	Pro
				515					520					525	
Leu	Ala	Ala	Ile	Ile	Gly	Gly	Ala	Val	Ala	Leu	Val	Ser	Ile	Ala	Leu
				530					535					540	
Leu	Ala	Leu	Val	Cys	Trp	Tyr	Val	His	Arg	Asn	Gly	Ser	Leu	Phe	Ser

545	Arg	Asn	Cys	Ala	Tyr	550	Ser	Lys	Gly	Arg	Arg	Arg	Lys	Asp	Asp	555	Tyr	Ala	560
						565													
	Glu	Ala	Gly	Thr	Lys		Lys	Asp	Asn	Ser	Ile	Leu	Glu	Ile	Arg		Glu	Thr	
						580					585					590			
	Ser	Phe	Gln	Met	Leu		Pro	Ile	Ser	Asn	Glu	Pro	Ile	Ser	Lys		Glu	Glu	
						595				600				605					
	Phe	Val	Ile	His	Thr		Ile	Phe	Pro	Pro	Asn	Gly	Met	Asn	Leu	Tyr	Lys		
						610		615					620						
	Asn	Asn	Leu	Ser	Glu		Ser	Ser	Ser	Asn	Arg	Ser	Tyr	Arg	Asp	Ser	Gly		
						625		630				635					640		
	Ile	Pro	Asp	Ser	Asp		His	Ser	His	Ser									
						645													

<210> 306

<211> 150

<212> PRT

<213> Rat

<400> 306

Met	Ala	Ala	Pro	Met	Asp	Arg	Thr	His	Gly	Gly	Arg	Ala	Ala	Arg	Ala				
1				5					10					15					
Leu	Arg	Arg	Ala	Leu	Ala	Leu	Ala	Ser	Leu	Ala	Gly	Leu	Leu	Leu	Ser				
			20					25					30						
Gly	Leu	Ala	Gly	Ala	Leu	Pro	Thr	Leu	Gly	Pro	Gly	Trp	Arg	Arg	Gln				
			35				40					45							
Asn	Pro	Glu	Pro	Pro	Ala	Ser	Arg	Thr	Arg	Ser	Leu	Leu	Leu	Asp	Ala				
						55					60								
Ala	Ser	Gly	Gln	Leu	Arg	Leu	Glu	Tyr	Gly	Phe	His	Pro	Asp	Ala	Val				
65					70					75					80				
Ala	Trp	Ala	Asn	Leu	Thr	Asn	Ala	Ile	Arg	Glu	Thr	Gly	Trp	Ala	Tyr				
				85					90					95					
Leu	Asp	Leu	Gly	Thr	Asn	Gly	Ser	Tyr	Lys	Trp	Ile	Pro	Arg	Ala	Ala				
			100					105					110						
Gly	Leu	Cys	Ser	Trp	Cys	Gly	Gly	Gly	Leu	Cys	Val	Arg	Gly	Ala	His				
			115				120					125							
Leu	His	Ala	Leu	Asp	Glu	His	Gly	Gly	Gln	Leu	Leu	Arg	Pro	Leu	Arg				
			130			135					140								
Val	Arg	Ser	Arg	Leu	Leu														
145					150														

<210> 307

<211> 580

<212> PRT

<213> Rat

<400> 307

Met	Ala	Ala	Ala	Met	Pro	Leu	Gly	Leu	Ser	Leu	Leu	Leu	Leu	Val	Leu				
1				5					10					15					
Val	Gly	Gln	Gly	Cys	Cys	Gly	Arg	Val	Glu	Gly	Pro	Arg	Asp	Ser	Leu				
			20					25					30						
Arg	Glu	Glu	Leu	Val	Ile	Thr	Pro	Leu	Pro	Ser	Gly	Asp	Val	Ala	Ala				
			35				40					45							
Thr	Phe	Gln	Phe	Arg	Thr	Arg	Trp	Asp	Ser	Asp	Leu	Gln	Arg	Glu	Gly				
	50					55					60								
Val	Ser	His	Tyr	Arg	Leu	Phe	Pro	Lys	Ala	Leu	Gly	Gln	Leu	Ile	Ser				
65					70					75					80				
Lys	Tyr	Ser	Leu	Arg	Glu	Leu	His	Leu	Ser	Phe	Thr	Gln	Gly	Phe	Trp				
				85					90					95					
Arg	Thr	Arg	Tyr	Trp	Gly	Pro	Pro	Phe	Leu	Gln	Ala	Pro	Ser	Gly	Ala				
			100				105							110					

Glu	Leu	Trp	Val	Trp	Phe	Gln	Asp	Thr	Val	Thr	Asp	Val	Asp	Lys	Ser	115	120	125
Trp	Lys	Glu	Leu	Ser	Asn	Val	Leu	Ser	Gly	Ile	Phe	Cys	Ala	Ser	Leu	130	135	140
Asn	Phe	Ile	Asp	Ser	Thr	Asn	Thr	Val	Thr	Pro	Thr	Ala	Ser	Phe	Lys	145	150	155
Pro	Leu	Gly	Leu	Ala	Asn	Asp	Thr	Asp	His	Tyr	Phe	Leu	Arg	Tyr	Ala	165	170	175
Val	Leu	Pro	Arg	Glu	Val	Val	Cys	Thr	Glu	Asn	Leu	Thr	Pro	Trp	Lys	180	185	190
Lys	Leu	Leu	Pro	Cys	Ser	Ser	Lys	Ala	Gly	Leu	Ser	Val	Leu	Leu	Lys	195	200	205
Ala	Asp	Arg	Leu	Phe	His	Thr	Ser	Tyr	His	Ser	Gln	Ala	Val	His	Ile	210	215	220
Arg	Pro	Ile	Cys	Arg	Asn	Ala	His	Cys	Thr	Ser	Ile	Ser	Trp	Glu	Leu	225	230	235
Arg	Gln	Thr	Leu	Ser	Val	Val	Phe	Asp	Ala	Phe	Ile	Thr	Gly	Gln	Gly	245	250	255
Lys	Lys	Asp	Trp	Ser	Leu	Phe	Arg	Met	Phe	Ser	Arg	Thr	Leu	Thr	Glu	260	265	270
Ala	Cys	Pro	Leu	Ala	Ser	Gln	Ser	Leu	Val	Tyr	Val	Asp	Ile	Thr	Gly	275	280	285
Tyr	Ser	Gln	Asp	Asn	Glu	Thr	Leu	Glu	Val	Ser	Pro	Pro	Pro	Thr	Ser	290	295	300
Thr	Tyr	Gln	Asp	Val	Ile	Leu	Gly	Thr	Arg	Lys	Thr	Tyr	Ala	Val	Tyr	305	310	315
Asp	Leu	Phe	Asp	Thr	Ala	Met	Ile	Asn	Asn	Ser	Arg	Asn	Leu	Asn	Ile	325	330	335
Gln	Leu	Lys	Trp	Lys	Arg	Pro	Pro	Asp	Asn	Glu	Ala	Leu	Pro	Val	Pro	340	345	350
Phe	Leu	His	Ala	Gln	Arg	Tyr	Val	Ser	Gly	Tyr	Gly	Leu	Gln	Lys	Gly	355	360	365
Glu	Leu	Ser	Thr	Leu	Leu	Tyr	Asn	Ser	His	Pro	Tyr	Arg	Ala	Phe	Pro	370	375	380
Val	Leu	Leu	Leu	Asp	Ala	Val	Pro	Trp	Tyr	Leu	Arg	Leu	Tyr	Val	His	385	390	395
Thr	Leu	Thr	Ile	Thr	Ser	Lys	Gly	Lys	Asp	Asn	Lys	Pro	Ser	Tyr	Ile	405	410	415
His	Tyr	Gln	Pro	Ala	Gln	Asp	Arg	Gln	Gln	Pro	His	Leu	Leu	Glu	Met	420	425	430
Leu	Ile	Gln	Leu	Pro	Ala	Asn	Ser	Val	Thr	Lys	Val	Ser	Ile	Gln	Phe	435	440	445
Glu	Arg	Ala	Leu	Leu	Lys	Trp	Thr	Glu	Tyr	Thr	Pro	Asp	Pro	Asn	His	450	455	460
Gly	Phe	Tyr	Val	Ser	Pro	Ser	Val	Leu	Ser	Ala	Leu	Val	Pro	Ser	Met	465	470	475
Val	Ala	Ala	Lys	Pro	Val	Asp	Trp	Glu	Glu	Ser	Pro	Leu	Phe	Asn	Thr	485	490	495
Leu	Phe	Pro	Val	Ser	Asp	Gly	Ser	Ser	Tyr	Phe	Val	Arg	Leu	Tyr	Thr	500	505	510
Glu	Pro	Leu	Leu	Val	Asn	Leu	Pro	Thr	Pro	Asp	Phe	Ser	Met	Pro	Tyr	515	520	525
Asn	Val	Ile	Cys	Leu	Thr	Cys	Thr	Val	Val	Ala	Val	Cys	Tyr	Gly	Ser	530	535	540
Phe	Tyr	Asn	Leu	Leu	Thr	Arg	Thr	Phe	His	Ile	Glu	Glu	Pro	Lys	Ser	545	550	555
Gly	Gly	Leu	Ala	Lys	Arg	Leu	Ala	Asn	Leu	Ile	Arg	Arg	Ala	Arg	Gly	565	570	575
Val	Pro	Pro	Leu													580		

<210> 308
 <211> 283
 <212> PRT
 <213> Rat

<400> 308
 Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
 1 5 10 15
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
 20 25 30
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
 35 40 45
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
 50 55 60
 Tyr His Ser Phe Val Ser Ser Val Phe Ser Leu Phe Met Ser Arg Thr
 65 70 75 80
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
 85 90 95
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
 100 105 110
 Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
 115 120 125
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
 130 135 140
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
 145 150 155 160
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
 165 170 175
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Ser
 180 185 190
 Val Leu Glu Pro Thr Gln Gly Arg Val Ile Leu Ala Leu Val Leu Pro
 195 200 205
 Phe His Pro Tyr Val Glu Asn Val Gly Gly Lys Trp Glu Lys Pro Ser
 210 215 220
 Glu Ile Leu Glu Ile Lys Gly Gln Asn Trp Glu Glu Gln Val Asn Ser
 225 230 235 240
 Leu Pro Glu Val Phe Arg Lys Ala Gly Phe Val Ile Glu Ala Phe Thr
 245 250 255
 Arg Leu Pro Tyr Leu Cys Glu Gly Asp Met Tyr Asn Asp Tyr Tyr Val
 260 265 270
 Leu Asp Asp Ala Val Phe Val Leu Arg Pro Val
 275 280

<210> 309
 <211> 37
 <212> PRT
 <213> Rat

<400> 309
 Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
 1 5 10 15
 Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
 20 25 30
 Arg Ala Asp Val Leu
 35

<210> 310
 <211> 70
 <212> PRT
 <213> Mouse

<400> 310

Met Ala Ala Ser Trp Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala
 1 5 10 15
 Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ser Gly Leu
 20 25 30
 Glu Gln Val Arg Glu Arg Thr Trp Ala Trp Gln Leu Leu Gln Glu Ile
 35 40 45
 Lys Ala Leu Phe Gly Asn Thr Glu Val Arg Leu Ala Leu Thr Asp Glu
 50 55 60
 Pro Leu Lys Ile Ser Pro
 65 70

<210> 311

<211> 58

<212> PRT

<213> Human

<400> 311

Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
 1 5 10 15
 Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
 20 25 30
 Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
 35 40 45
 Gln Glu Pro Gln Gly Lys Ala Lys Arg His
 50 55

<210> 312

<211> 52

<212> PRT

<213> Human

<400> 312

Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys
 1 5 10 15
 Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser
 20 25 30
 Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu
 35 40 45
 Glu Lys Thr Lys
 50

<210> 313

<211> 70

<212> PRT

<213> Human

<400> 313

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1 5 10 15
 Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
 20 25 30
 Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
 35 40 45
 Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
 50 55 60
 Pro Met Thr Pro Pro Trp
 65 70

<210> 314

<211> 58

<212> PRT

<213> Mouse

<400> 314

Met Phe Ile Thr Pro Phe Lys Ala Phe Leu Pro Leu Tyr Leu Leu Thr
 1 5 10 15
 Glu Leu Ser Leu Ile Asp Ile Thr Ser Cys Asp Asp Leu Pro His Ser
 20 25 30
 Val Leu Pro Gln His Leu Ser Phe Glu Phe Val Leu Trp Ser Met Tyr
 35 40 45
 Leu Leu Ile Cys Cys Phe Val Ile Ile Phe
 50 55

<210> 315

<211> 229

<212> PRT

<213> Rat

<400> 315

Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1 5 10 15
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20 25 30
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35 40 45
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50 55 60
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65 70 75 80
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85 90 95
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
 100 105 110
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
 115 120 125
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
 130 135 140
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
 145 150 155 160
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
 165 170 175
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
 180 185 190
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys
 195 200 205
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
 210 215 220
 Glu Asp Thr Glu Phe
 225

<210> 316

<211> 128

<212> PRT

<213> Rat

<400> 316

Arg Ala Glu Phe Gly Thr Ser Gly Glu Met Gly Asn Ala Ala Leu Gly
 1 5 10 15
 Ala Glu Leu Gly Val Arg Val Leu Leu Phe Val Ala Phe Leu Ala Thr
 20 25 30
 Glu Leu Leu Pro Pro Phe Gln Arg Arg Ile Gln Pro Glu Glu Leu Trp

35 40 45
 Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Gly Pro
 50 55 60
 Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile Phe Phe Ala
 65 70 75 80
 Lys Phe Leu Arg Lys Ala Asp Ala Thr Asp Ser Lys Gln Ala Cys Leu
 85 90 95
 Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Ile Ile
 100 105 110
 Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe
 115 120 125

<210> 317
 <211> 75
 <212> PRT
 <213> Rat

<400> 317
 Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
 1 5 10 15
 Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
 20 25 30
 Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
 35 40 45
 Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
 50 55 60
 Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
 65 70 75

<210> 318
 <211> 43
 <212> PRT
 <213> Human

<400> 318
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
 1 5 10 15
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
 20 25 30
 Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
 35 40

<210> 319
 <211> 86
 <212> PRT
 <213> Mouse

<400> 319
 Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
 1 5 10 15
 Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
 20 25 30
 Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
 35 40 45
 Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly
 50 55 60
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
 65 70 75 80
 Leu Leu Ser Phe Pro Pro
 85

<210> 320
 <211> 60
 <212> PRT
 <213> Mouse

<400> 320
 Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe
 1 5 10 15
 Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu
 20 25 30
 Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr
 35 40 45
 Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu
 50 55 60

<210> 321
 <211> 160
 <212> PRT
 <213> Mouse

<400> 321
 Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala
 1 5 10 15
 Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu
 20 25 30
 Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro
 35 40 45
 Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu
 50 55 60
 Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu
 65 70 75 80
 Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly
 85 90 95
 Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe
 100 105 110
 Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val
 115 120 125
 Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr
 130 135 140
 Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Ser Ser
 145 150 155 160

<210> 322
 <211> 54
 <212> PRT
 <213> Mouse

<400> 322
 Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Val Leu Phe Leu Phe Phe
 1 5 10 15
 Phe Phe Phe Leu Cys Val Cys Val Leu Val Cys Cys Cys Phe Gly Phe
 20 25 30
 Pro Gly Thr His Ser Val Asp Gln Ala Ser Pro Lys Leu Arg Asn Leu
 35 40 45
 Pro Pro Glu Cys Trp Asp
 50

<210> 323
 <211> 280
 <212> PRT
 <213> Mouse

<400> 323

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Leu Asp Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser
 1          5          10          15
Ala Arg Glu Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile
          20          25          30
Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile
          35          40          45
Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro
 50          55          60
His His His His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu
65          70          75          80
Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val
          85          90          95
Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg
          100          105          110
Lys Phe Val His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala
          115          120          125
Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe
130          135          140
Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala
145          150          155          160
Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met
          165          170          175
Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp
          180          185          190
Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly
          195          200          205
Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp
210          215          220
Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys
225          230          235          240
Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu
          245          250          255
Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys
          260          265          270
Ala Met Pro Ser Asp Met Asp Ser
          275          280

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<210> 324

<211> 166

<212> PRT

<213> Rat

<400> 324

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Ala Leu Arg Arg Val Gly Met Glu Leu Pro Ala Val Asn Leu Lys Val
 1          5          10          15
Ile Leu Leu Val His Trp Leu Leu Thr Thr Trp Gly Cys Leu Ala Phe
          20          25          30
Ser Gly Ser Tyr Ala Trp Gly Asn Phe Thr Ile Leu Ala Leu Gly Val
          35          40          45
Trp Ala Val Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu
 50          55          60
Gly Gly Leu Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile
65          70          75          80
Phe Tyr Ser Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly
          85          90          95
Met Ala Ile Phe Ser Leu Leu Leu Lys Pro Phe Ser Cys Cys Leu Val
          100          105          110
Tyr His Met His Arg Glu Arg Gly Gly Glu Leu Pro Leu Arg Ser Asp
115          120          125

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Phe Phe Gly Pro Ser Gln Glu His Ser Ala Tyr Gln Thr Ile Asp Ser
 130 135 140
 Ser Asp Ser Pro Ala Asp Pro Leu Ala Ser Leu Glu Asn Lys Gly Gln
 145 150 155 160
 Ala Ala Pro Arg Gly Tyr
 165

<210> 325

<211> 338

<212> PRT

<213> Rat

<400> 325

Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala
 1 5 10 15
 Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu
 20 25 30
 Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro
 35 40 45
 Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu
 50 55 60
 Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu
 65 70 75 80
 Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly
 85 90 95
 Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe
 100 105 110
 Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val
 115 120 125
 Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr
 130 135 140
 Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Met Phe
 145 150 155 160
 Ile Val Cys Ala Ala Leu Ile Thr Arg Gln Lys His Lys Ala Thr Ala
 165 170 175
 Tyr Tyr Pro Ser Ser Phe Pro Glu Lys Lys Tyr Val Asp Gln Arg Asp
 180 185 190
 Arg Ala Gly Gly Pro His Ala Phe Ser Glu Val Pro Asp Arg Ala Pro
 195 200 205
 Asp Ser Arg Gln Glu Glu Gly Leu Asp Ser Ser Gln Gln Leu Gln Ala
 210 215 220
 Asp Ile Leu Ala Ala Thr Gln Asn Leu Arg Ser Pro Ala Arg Ala Leu
 225 230 235 240
 Pro Gly Ser Gly Glu Gly Thr Lys Gln Val Lys Gly Gly Ser Glu Glu
 245 250 255
 Glu Glu Glu Lys Glu Glu Glu Val Phe Ser Gly Gln Glu Glu Pro Arg
 260 265 270
 Glu Ala Pro Val Cys Gly Val Thr Glu Glu Lys Pro Glu Val Pro Asp
 275 280 285
 Glu Thr Ala Ser Ala Glu Ala Glu Gly Val Pro Ala Ala Ser Glu Gly
 290 295 300
 Gln Gly Glu Pro Glu Gly Ser Phe Ser Leu Ala Gln Glu Pro Gln Gly
 305 310 315 320
 Ala Ala Gly Pro Ser Glu Arg Ser Cys Ala Cys Asn Arg Ile Ser Pro
 325 330 335
 Asn Val

<210> 326

<211> 347

<212> PRT

<213> Human

<400> 326

Ala Trp Ser Arg Pro Arg Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala
 1 5 10 15
 Trp Gly Ile Val Leu Glu Thr Val Ala Thr Ala Gly Val Val Thr Ser
 20 25 30
 Val Ala Phe Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp
 35 40 45
 Ser Asn Arg Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly
 50 55 60
 Val Leu Gly Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp
 65 70 75 80
 Gly Ser Thr Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser
 85 90 95
 Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu
 100 105 110
 Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala
 115 120 125
 Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val
 130 135 140
 Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser Ala
 145 150 155 160
 Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Leu Thr Tyr Val Leu Phe
 165 170 175
 Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser
 180 185 190
 Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu
 195 200 205
 Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro
 210 215 220
 Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala
 225 230 235 240
 Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp
 245 250 255
 Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala
 260 265 270
 Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg
 275 280 285
 Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp
 290 295 300
 Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro
 305 310 315 320
 Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro
 325 330 335
 Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser
 340 345

<210> 327

<211> 141

<212> PRT

<213> Human

<400> 327

Lys Asn Ser Lys Cys Leu Leu Phe Trp Cys Arg Lys Ile Val Gly Asn
 1 5 10 15
 Arg Gln Glu Pro Met Trp Glu Phe Asn Phe Lys Phe Lys Lys Gln Ser
 20 25 30
 Pro Arg Leu Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln
 35 40 45
 Tyr Glu Asp Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln

50 55 60
 Val Thr Thr Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile
 65 70 75 80
 Phe Thr Leu Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg
 85 90 95
 Val Arg Leu Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu
 100 105 110
 Arg Ser Glu Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe
 115 120 125
 Gly Ser Leu Thr Gly Gly Ile Leu Ser Thr His Ser Pro
 130 135 140

<210> 328
 <211> 71
 <212> PRT
 <213> Human

<400> 328
 Arg Glu Arg Thr Ser Leu Glu Phe Phe Val Phe Leu Phe Leu Phe Ile
 1 5 10 15
 Cys Cys Cys Leu His Ser Gly Gly Leu Gly Gly Val Pro Leu Pro Pro
 20 25 30
 Phe Pro Pro Gln Ala Gln Arg Gly Glu Gly Pro Gly Lys Trp Met Ser
 35 40 45
 Pro Pro Leu Pro Pro His Pro Val Val Ala Pro Pro Thr Pro Ser Pro
 50 55 60
 Ser Arg Gly Cys Val Leu Leu
 65 70

<210> 329
 <211> 109
 <212> PRT
 <213> Human

<400> 329
 Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu Pro Ser Pro Ala Pro
 1 5 10 15
 Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly Leu Ala Glu His Ser
 20 25 30
 Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
 35 40 45
 Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
 50 55 60
 Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
 65 70 75 80
 Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro Arg
 85 90 95
 Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
 100 105

<210> 330
 <211> 155
 <212> PRT
 <213> Human

<400> 330
 Ser Val Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
 1 5 10 15
 Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
 20 25 30
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys

35	40	45
Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu		
50	55	60
Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys		
65	70	75
Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly		
85	90	95
Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro		
100	105	110
Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val		
115	120	125
Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe		
130	135	140
Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu		
145	150	155

<210> 331
 <211> 299
 <212> PRT
 <213> Human

<400> 331

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile	
1	5
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His	
20	25
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu	
35	40
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe	
50	55
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr	
65	70
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe	
85	90
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser	
100	105
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val	
115	120
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr	
130	135
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro	
145	150
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn	
165	170
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro	
180	185
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly	
195	200
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser	
210	215
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val	
225	230
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly	
245	250
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly	
260	265
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu	
275	280
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val	
290	295

<210> 332
 <211> 299
 <212> PRT
 <213> Mouse

<400> 332
 Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
 1 5 10 15
 Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
 20 25 30
 Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr
 35 40 45
 Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
 50 55 60
 Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg
 65 70 75 80
 Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
 85 90 95
 Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
 100 105 110
 Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
 115 120 125
 Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
 130 135 140
 Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
 145 150 155 160
 Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
 165 170 175
 Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
 180 185 190
 Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys
 195 200 205
 Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
 210 215 220
 Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
 225 230 235 240
 Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
 245 250 255
 Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
 260 265 270
 Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
 275 280 285
 Pro Gln His Ser Ser Ser Lys Ala Met Lys His
 290 295

<210> 333
 <211> 109
 <212> PRT
 <213> Mouse

<400> 333
 Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
 1 5 10 15
 Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
 20 25 30
 Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
 35 40 45
 Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
 50 55 60
 Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
 65 70 75 80

Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr
 85 90 95
 Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
 100 105

<210> 334
 <211> 787
 <212> PRT
 <213> Mouse

<400> 334
 Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
 1 5 10 15
 Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
 20 25 30
 Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
 35 40 45
 Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
 50 55 60
 Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
 65 70 75 80
 Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
 85 90 95
 Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
 100 105 110
 Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
 115 120 125
 Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
 130 135 140
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile
 145 150 155 160
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp
 165 170 175
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu
 180 185 190
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr
 195 200 205
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe
 210 215 220
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly
 225 230 235 240
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys
 245 250 255
 Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro Gln
 260 265 270
 Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys
 275 280 285
 Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu
 290 295 300
 Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg
 305 310 315 320
 Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser
 325 330 335
 Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly
 340 345 350
 Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro Ser Ser
 355 360 365
 Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe
 370 375 380
 Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr
 385 390 395 400

Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala
 405 410 415
 Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln
 420 425 430
 Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala
 435 440 445
 Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn
 450 455 460
 Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met
 465 470 475 480
 Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg
 485 490 495
 Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His
 500 505 510
 Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu
 515 520 525
 Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met
 530 535 540
 His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu
 545 550 555 560
 Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro
 565 570 575
 Leu His Tyr Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Leu
 580 585 590
 Ala Lys Gln Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg
 595 600 605
 Thr Pro Leu His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg
 610 615 620
 Ile Leu Ile Asp Leu Cys Ser Asp Val Asn Ile Cys Ser Leu Gln Ala
 625 630 635 640
 Gln Thr Pro Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala
 645 650 655
 Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu Ala Leu Thr Ser Glu
 660 665 670
 Gly Tyr Thr Ala Leu His Leu Ala Ala Gln Asn Gly His Leu Ala Thr
 675 680 685
 Val Lys Leu Leu Ile Glu Glu Lys Ala Asp Val Met Ala Arg Gly Pro
 690 695 700
 Leu Asn Gln Thr Ala Leu His Leu Ala Ala Ala Arg Gly His Ser Glu
 705 710 715 720
 Val Val Glu Glu Leu Val Ser Ala Asp Leu Ile Asp Leu Ser Asp Glu
 725 730 735
 Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ser Gln
 740 745 750
 Thr Val Glu Thr Leu Leu Lys His Gly Ala His Ile Asn Leu Gln Ser
 755 760 765
 Leu Lys Phe Gln Gly Gly Gln Ser Ser Ala Ala Thr Leu Leu Arg Arg
 770 775 780
 Ser Lys Thr
 785

<210> 335
 <211> 194
 <212> PRT
 <213> Mouse

<400> 335
 Pro Gly Cys Lys Ser Cys Thr Val Cys Arg His Gly Leu Cys Arg Ser
 1 5 10 15
 Val Glu Lys Asp Ser Val Val Cys Glu Cys His Pro Gly Trp Thr Gly
 20 25 30

Pro Leu Cys Asp Gln Glu Ala Arg Asp Pro Cys Leu Gly His Ser Cys
 35 40 45
 Arg His Gly Thr Cys Met Ala Thr Gly Asp Ser Tyr Val Cys Lys Cys
 50 55 60
 Ala Glu Gly Tyr Gly Gly Ala Leu Cys Asp Gln Lys Asn Asp Ser Ala
 65 70 75 80
 Ser Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 85 90 95
 Asp Arg Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly His
 100 105 110
 His Cys Glu Gln Glu Asn Pro Cys Met Gly Glu Ile Val Arg Glu Ala
 115 120 125
 Ile Arg Arg Gln Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val
 130 135 140
 Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro
 145 150 155 160
 Ile Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly Ser
 165 170 175
 Ser Phe Val Glu Glu Val Glu Arg His Leu Glu Cys Gly Cys Arg Ala
 180 185 190
 Cys Ser

<210> 336
 <211> 274
 <212> PRT
 <213> Human

<400> 336
 Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu Pro Gly Ser Phe Arg
 1 5 10 15
 Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro Asn Asn Arg Ser Cys
 20 25 30
 Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro Cys Glu Gln Arg Cys
 35 40 45
 Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys His Gln Gly Tyr Glu
 50 55 60
 Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile Asp Glu Cys Ser Tyr
 65 70 75 80
 Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn Glu Pro Gly Arg Phe
 85 90 95
 Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu Ala Thr Arg Leu Cys
 100 105 110
 Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His Gln Cys Ser Glu Ala
 115 120 125
 Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg Cys Val Asp Thr Asn
 130 135 140
 Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu Asn Arg Cys Leu Cys
 145 150 155 160
 Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro Ser Ser Ile Val His
 165 170 175
 Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val Pro Ala Asp Val Phe
 180 185 190
 Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala Tyr Asn Ala Phe Gln
 195 200 205
 Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr Ile Arg Gln Ile Asn
 210 215 220
 Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro Val Thr Gly Pro Arg
 225 230 235 240
 Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met Asn Ser Leu Met Ser
 245 250 255

Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val Phe Val Gly Ala Tyr
 260 265 270
 Thr Phe

<210> 337
 <211> 316
 <212> PRT
 <213> Mouse

<400> 337
 His Glu Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn
 1 5 10 15
 Ile Asp Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His
 20 25 30
 Val Met Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln
 35 40 45
 Ala Ile Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala
 50 55 60
 Lys Thr Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala
 65 70 75 80
 Ser Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys
 85 90 95
 Thr His Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg
 100 105 110
 Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys
 115 120 125
 Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala
 130 135 140
 Met Ser Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser
 145 150 155 160
 Thr Thr Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln
 165 170 175
 Leu Glu Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met
 180 185 190
 Arg Gly Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp
 195 200 205
 Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile
 210 215 220
 Ser Gly Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys
 225 230 235 240
 Arg Arg Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro
 245 250 255
 Ser Ala Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp
 260 265 270
 Leu Gly Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp
 275 280 285
 Glu Gln Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile
 290 295 300
 Leu Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
 305 310 315

<210> 338
 <211> 237
 <212> PRT
 <213> Mouse

<400> 338
 Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1 5 10 15
 Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser

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<210> 339
<211> 469
<212> PRT
<213> Mouse
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136

210	215	220
Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys		
225	230	235
Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu		
245	250	255
Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly		
260	265	270
Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser		
275	280	285
Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu		
290	295	300
Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu		
305	310	315
Asp Cys Ala Arg Arg Ile Leu Ala Lys Glu Gly Val Ala Ala Phe Tyr		
325	330	335
Lys Gly Tyr Ile Pro Asn Met Leu Gly Ile Ile Pro Tyr Ala Gly Ile		
340	345	350
Asp Leu Ala Val Tyr Glu Thr Leu Lys Asn Thr Trp Leu Gln Arg Tyr		
355	360	365
Ala Val Asn Ser Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly		
370	375	380
Thr Ile Ser Ser Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu		
385	390	395
Val Arg Thr Arg Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu		
405	410	415
Val Thr Met Ser Ser Leu Phe Lys Gln Ile Leu Arg Thr Glu Gly Ala		
420	425	430
Phe Gly Leu Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro		
435	440	445
Ala Val Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu		
450	455	460
Gly Val Gln Ser Arg		
465		

<210> 340
 <211> 99
 <212> PRT
 <213> Mouse

<400> 340
Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Cys
1 5 10 15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
20 25 30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
35 40 45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
50 55 60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
65 70 75 80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
85 90 95
Tyr Glu Glu

<210> 341
 <211> 431
 <212> PRT
 <213> Mouse

<400> 341

Met	Asp	Ala	Arg	Trp	Trp	Ala	Val	Val	Val	Leu	Ala	Thr	Leu	Pro	Ser
1				5					10					15	
Leu	Gly	Ala	Gly	Gly	Glu	Ser	Pro	Glu	Ala	Pro	Pro	Gln	Ser	Trp	Thr
			20					25					30		
Gln	Leu	Trp	Leu	Phe	Arg	Phe	Leu	Leu	Asn	Val	Ala	Gly	Tyr	Ala	Ser
		35					40					45			
Phe	Met	Val	Pro	Gly	Tyr	Leu	Leu	Val	Gln	Tyr	Leu	Arg	Arg	Lys	Asn
	50					55					60				
Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys
65					70					75					80
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Pro	Asp	Glu	Val	Leu	Leu	Ala	Pro
			85						90					95	
Arg	Thr	Glu	Thr	Ala	Glu	Ser	Thr	Pro	Ser	Trp	Gln	Val	Leu	Lys	Leu
			100					105					110		
Val	Phe	Cys	Ala	Ser	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Ile
		115					120					125			
Leu	Gln	Glu	Arg	Val	Met	Thr	Gly	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser
		130				135					140				
Pro	Gly	Glu	His	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg
145					150					155					160
Val	Leu	Ala	Leu	Val	Val	Ala	Gly	Leu	Tyr	Cys	Val	Leu	Arg	Lys	Gln
			165						170					175	
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser
			180					185					190		
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser
		195					200					205			
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met
		210				215					220				
Met	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr
225					230					235					240
Leu	Thr	Ala	Gly	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser
			245					250						255	
Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	Gly	Leu
			260					265				270			
Val	Leu	Leu	Ala	Gly	Tyr	Ile	Ala	Phe	Asp	Ser	Phe	Thr	Ser	Asn	Trp
		275					280					285			
Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Lys	Met	Ser	Ser	Val	Gln	Met	Met	Phe
	290					295					300				
Gly	Val	Asn	Leu	Phe	Ser	Cys	Leu	Phe	Thr	Val	Gly	Ser	Leu	Leu	Glu
305					310					315					320
Gln	Gly	Ala	Leu	Leu	Glu	Gly	Ala	Arg	Phe	Met	Gly	Arg	His	Ser	Glu
			325					330						335	
Phe	Ala	Leu	His	Ala	Leu	Leu	Leu	Ser	Ile	Cys	Ser	Ala	Phe	Gly	Gln
			340					345					350		
Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly	Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr
		355					360					365			
Ile	Ile	Met	Thr	Leu	Arg	Gln	Ala	Ile	Ala	Ile	Leu	Leu	Ser	Cys	Leu
		370				375					380				
Leu	Tyr	Gly	His	Thr	Val	Thr	Val	Val	Gly	Gly	Leu	Gly	Val	Ala	Val
385					390					395					400
Val	Phe	Thr	Ala	Leu	Leu	Leu	Arg	Val	Tyr	Ala	Arg	Gly	Arg	Lys	Gln
			405					410						415	
Arg	Gly	Lys	Lys	Ala	Val	Pro	Thr	Glu	Pro	Pro	Val	Gln	Lys	Val	
			420					425					430		

<210> 342
 <211> 51
 <212> PRT
 <213> Mouse

<400> 342

Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
 1 5 10 15
 Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln Ala Ile Cys Arg
 20 25 30
 Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His Leu Thr Leu Thr
 35 40 45
 Ser Tyr Ala
 50

<210> 343
 <211> 51
 <212> PRT
 <213> Human
 <400> 343

Leu Lys Phe Ser His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
 1 5 10 15
 Asn Gly Ala Cys Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg
 20 25 30
 Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu His Leu Thr Leu Thr
 35 40 45
 Ser Tyr Ala
 50

<210> 344
 <211> 95
 <212> PRT
 <213> Human

<400> 344

Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala Arg Val
 1 5 10 15
 Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr
 20 25 30
 Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu
 35 40 45
 Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly
 50 55 60
 Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile
 65 70 75 80
 Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 85 90 95

<210> 345
 <211> 77
 <212> PRT
 <213> Mouse

<400> 345

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
 1 5 10 15
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
 20 25 30
 Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu
 35 40 45
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
 50 55 60
 Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 65 70 75

<210> 346
 <211> 77

<212> PRT
<213> Human

<400> 346
Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
1 5 10 15
Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
20 25 30
Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu
35 40 45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
50 55 60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65 70 75

<210> 347
<211> 215
<212> PRT
<213> Mouse

<400> 347
Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
1 5 10 15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
20 25 30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
35 40 45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
50 55 60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
65 70 75 80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
85 90 95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
100 105 110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
115 120 125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
130 135 140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145 150 155 160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
165 170 175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
180 185 190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
195 200 205
Lys Ser Leu Ala Ile Arg Thr
210 215

<210> 348
<211> 21
<212> PRT
<213> Mouse

<400> 348
Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly Ser Lys Val
1 5 10 15
Pro Gln Phe Leu Asn

<210> 349

<211> 417
 <212> DNA
 <213> Mouse

<400> 349

gctagccgtg	cacccagctc	tccggagcgc	gtgcaggcga	gccgagcgcc	ccgtccgcgg	60
ttctcgggca	ggcgtgcgg	gctccccggc	tccccgccgt	cccgggcacc	cgggcgggcc	120
atgcgcccgg	gctagagcgt	agccgcccgg	atgcgcctcc	cgctgctgct	cgccgcgctc	180
tgcctcgccg	cctccccggc	gcccgcgcgc	gcctgccagc	tgccgtcggg	gtggagaccc	240
ttgagcgaag	gctgccgcgc	cgagctagcc	gagaccatcg	tgtatgccaa	ggtgctggcg	300
ctgcaccccg	aggtgcctgg	cctctacaac	tacctgccgt	ggcagtacca	agctggagag	360
ggagggctct	tctactccgc	cgaggtggag	atgcttgtgt	gaccaaggcg	tggggca	417

<210> 350
 <211> 1837
 <212> DNA
 <213> Mouse

<400> 350

ccccacctg	cccagccaag	ccgagtgccg	ccggetttgt	tcgctttgtc	ctcgcgccacc	60
taagcggccg	gcctggaaga	acgccatccc	ggagagcgca	cgcggcgtcg	caccaggtct	120
aacaacatgc	ctccacttct	gcttctacca	gccatctaca	tgctcctgtt	cttcagagtg	180
tccccgacca	tctctcttca	ggaagtgcac	gtgaaccggg	agaccatggg	gaagatcgct	240
gtggccagca	aattaatgtg	gtgctcagcc	gcggtcgaca	tcctgtttct	gttagatggc	300
tctcacagca	tcgggaaggg	gagcttcgag	aggtccaagc	gcttcgccat	cgctgcctgt	360
gatgccctgg	acatcagccc	tggcagggtc	agagtcggag	ccttgagttt	tggttccact	420
cctcatctgg	aattccccct	ggactccttc	tcaactcgac	aggaagtga	ggaaagcatc	480
aaggggatag	ttttcaaagg	tgggcgcacc	gagacggggc	tagccctgaa	acgcctgagc	540
agagggttcc	ccggaggcag	aaatggctct	gtgccccaga	ttcttatcat	cgtcacggat	600
ggcaagtccc	aggggcccgt	ggctctcccc	gctaagcagc	tgagagaaa	gggcatcgct	660
gtgtttgccg	taggagtcgg	ttttcccagg	tgggacgagc	tgctcacgct	ggccagtggg	720
ccgaaggacc	ggcatgtgct	gttggctgag	caagtggagg	atgccaccaa	tggcctcctc	780
agcacctcca	gcagctccgc	actctgcacc	actgctgac	cagactgcag	ggtggaacct	840
catccctgtg	agcggaggac	gctggagacc	gtcagggagc	tcgctggcaa	tgccttgtgc	900
tggagaggat	caaggcaagc	agacactgtg	ctggctctgc	cctgtccctt	ctacagctgg	960
aagagagtgt	tccagacaca	ccctgccaac	tgctacagaa	ccatctgtcc	aggcccctgt	1020
gactcccagc	cctgccaaaa	tggaggcacg	tgcatccag	aaggtgtgga	taggtaccac	1080
tgtctctgcc	cactggcatt	cggaggggaa	gtcaactgtg	ccccgaagct	gagcctggaa	1140
tgcagaatcg	atgtcctctt	cctgctggac	agttctgcag	gcaccacatt	ggggggcttc	1200
cggagggcca	aggcctttgt	caagcgcttt	gtgcaggccg	tgctgaggga	ggactccoga	1260
gcccgcgttg	ggatagccag	ttatggcagg	aatctaattg	tggcggtgcc	ctgtcgggga	1320
gtaccagcat	tgtgccggac	ctgatcagga	gccttgacag	cattcccttc	agcgggtggc	1380
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ctctgtggga	cgtgagaact	ttgccc aaat	gcagagcttc	atcaggaaat	gcaccctccg	1800
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<210> 351
 <211> 941
 <212> DNA
 <213> Mouse

<400> 351

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ggtggtagca	ggcgtggtgg	cgctgactct	agccctggtc	ctagcctggc	tctccaccta	180
tgtagcagac	agtggtaaca	accagctgct	gggcaccatt	gtgtcagcag	gtgacacgtc	240

tggtctccac	ctgggccatg	tggaccagct	ggtaaaccac	ggcactccag	agccaaccga	300
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caagtccctc	aatgacacgg	aggagctagc	tgtggccagg	ccagaggaca	ctgtgggtac	600
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aatgaagttg	atctaccagg	gtcggctgct	gcaggaccca	gcacgcacac	tgagttccct	900
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<210> 352

<211> 571

<212> DNA

<213> Mouse

<400> 352

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atgttgatgt	cttttggttc	cgtgaacaag	tagaaattgc	atgtgtctac	cggtgacagt	180
gtggtgtcac	tgggccctgt	gggtggctca	cttacctctg	attccgtctg	tgggaaagtc	240
ccagtgtacc	caaatgtggc	attgttgcat	gccttggggtg	tgtgtgggag	attgtctctg	300
tctctcagac	cctttgtggc	tttgtctgtt	gaaagagaca	gagaccctt	gtggttttct	360
cagctgagaa	ccctccctcc	tgggatgttg	gggtgaaact	taactgcttt	gcaaagcctg	420
cccctcctca	tgctgacctt	tcaatatctg	gcagtgcatt	gttcccaagc	ccccttgtc	480
atattgggaatg	tcagggtctt	ctcaccttga	cagctgataa	ttccattcct	cgactcttga	540
gaactggccc	ttgctttgtt	ttctctgcct	g			571

<210> 353

<211> 467

<212> DNA

<213> Rat

<400> 353

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catggtgcgc	caggccccga	aggcaccgcg	cccagacccg	cccactacag	ggagcgagtc	180
aaggccatgt	tctaccacgc	ctacgacagt	tacctgaaa	atgcctttcc	ctacgatgag	240
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gatgccttgg	acaccttgct	gattttgggg	aatacctctg	aattccaaag	agtgggtggag	360
gttctccagg	acaaacgtgg	actttgatat	cgacgtcaat	gcctctgtgt	tcgaaaccaa	420
catccgagtg	gtaggaggac	tcctttctgc	tcattctctt	tcaaaga		467

<210> 354

<211> 528

<212> DNA

<213> Rat

<400> 354

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tctcgagttg	ccactcccaa	gccagccccc	actggccata	tggcatcata	tctgggggtc	180
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tatcctgttg	ttaagctgtt	tccacagaag	cccgttcagg	tagttacttc	acccacattg	420
gccctatagc	cagaggagtg	ccctggctaa	ctgcagtggtg	agcttgtaag	caacagaagt	480
gcccaggagc	tgaccccaaa	ggccaggaag	gctcgagctt	gccacttt		528

<210> 355
 <211> 473
 <212> DNA
 <213> Mouse

<400> 355
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 ggcatttgtt gcgtctttcc tcctgtggcc ttcagcactg ataagaatct attattggta 180
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 ttactccttc cggggcaggc caggacacaa gccatccatc cttatgctcc atggattctc 300
 cgcacacaag gacatgtggc tcagcgtggg caagtctctt ccgaagaacc tgcacttggg 360
 ctgtgtggac atgcctgggc atgaaggcac caccgctcc tcctgggatg acctgtccat 420
 agtggggcaa gttaaaagga tacatcagtt tgtagaatgc cttaagctga aca 473

<210> 356
 <211> 431
 <212> DNA
 <213> Rat

<400> 356
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 caacctaaaa ccaaatggaa atggccggag agctccaggg cacctagggt ccctggcttc 120
 ggcttcggct gggctaacgc gcgagtgtgg tgggactatc ctaggagggtg ttcttgaga 180
 gagaggcgat ggcgtcaagt agtaactggc tgtccggagt gaatgtcgtt cttgtgatgg 240
 cgtacgggag cctgggtattc gtattgctgt ttatttttgt gaagagacaa atcatgcgct 300
 ttgcaatgaa atctagaagg ggacctcatg tccctgtggg acacaatgcc ccgaaggact 360
 taaaagagga aattgatatt cggctatcca gagttcagga catcaagtat gaaccgcagc 420
 tccttgcgaga t 431

<210> 357
 <211> 1206
 <212> DNA
 <213> Mouse

<400> 357
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 tggctccagc agggcagaga ggccacctgc agtctgggtg tgaagactcg tgtcagccgg 180
 gaggagtgtc gtgcttccgg caacatcaac accgcctggg ccaacttcac ccaccaggc 240
 aataaaatca gcctgctagg gttcctgggc ctgctccact gcctcccctg caaagattcc 300
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 ctgcgaagtt gcgtgcccga ctgcgagggg yttcccgcgg gcttccagggt ctgcggctct 420
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 cggcaccag gcactctgcac aggtggcccc aaagtaccag cagaggagga agagaacttc 780
 gtgtgagctg cagccactgg gcctggcatt tgacgccatc ccgattttat ttattgttat 840
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 gagctgtcgc agggcacagc cgatgagttg gtgtttgcat atggctggcc tcagaccaga 1140
 gcgggcaaca tcaggtcaga gaaacactgg gctcattcct gtttggtcca ctcagggtga 1200
 aacctg 1206

<210> 358
 <211> 1052
 <212> DNA

<213> Rat

<400> 358

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ctcttggcct	gtgcccttcc	gtgtgctgct	gacccaatgc	ttggtgcctt	tgctcgcagg	120
gacttccaga	aggggtggtcc	tcaactggtg	tgagctctgc	ctgggtcccca	aggccacctg	180
gccctccagg	agcaccagga	tcctcaggaa	tggtgggaag	aatgggtttt	cctggtaagg	240
atggccaaga	cggccaggac	ggagaccgag	gggacagtgg	agaagaagg	ccacctggca	300
ggacaggcaa	ccgaggaaaa	caaggaccaa	agggcaaagc	tggggccatt	gggagagcgg	360
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agggacctaa	gggcaagaaa	ggggaacctg	ggctcccagg	cccctgtagc	tgccgcagta	480
gccgagccaa	gtcggccttt	tcgggtggcg	taaccaagag	ttaccacagt	gagcgactgc	540
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aacacctggc	catcggccta	gtgcacaatg	gccagtaccg	cattcggact	tttgacgcca	720
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gaggatctct	gaactgaggc	tggggactgg	cagttcttgg	gagcttttat	tcccaggcaa	1020
gcctcctctg	gtgctgcttt	aaaaaaaaaa	aa			1052

<210> 359

<211> 1134

<212> DNA

<213> Rat

<400> 359

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gcggtggaag	cagagatggc	ggagggcggt	gggaggagag	gcgtctagtc	ttgctggctc	120
agcaagcccg	ataagcatga	agctgctgtg	tttgggtggc	gtgggtgggg	gcttgctggg	180
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cctgcatgtg	gtggagccca	tgccgggtgc	tgcccatgat	gtggaagcct	actgcctgct	360
ctgtgagtg	aggtatgagg	agcgcagcac	cacaaccatc	aaggtcatta	tcgtcatcta	420
cctgtctgtg	gtagggggccc	tcttactcta	catggccttc	ctgatgctgg	tggaacctct	480
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gtctttggtc	tctagtgtct	ctgtaggtct	ctggggtaga	agggagggaa	aggaaggcag	900
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gccgttcctc	acagctccac	atcttaagga	tgtttatagc	tctttggggag	acggagctgt	1020
gccgtcaata	gctcgggtggg	tgcgacgaaa	gtgtgaccca	gccctcagcc	tgtgctctac	1080
gatgccgtgg	ccccatttcc	cacttttnca	gtgccaatat	tttagcttgg	cctg	1134

<210> 360

<211> 876

<212> DNA

<213> Mouse

<400> 360

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gacatcagca	ccttggggaag	cctgcggcag	cttgatgtga	gcagcaatga	gctgcagtcc	120
ctgcccggtg	agctgtgtag	cctccgttcc	ctgcgggatc	tcaatgttcg	aaggaaccag	180
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ctggatagca	accccttaca	gagtcacact	gccagatat	gcctgaaggg	gaaacttcac	360
atcttcaagt	acctaacaat	ggaagctggc	cggagggggag	ccgcctcgg	ggacctggtc	420

ccttcccggc	ccccagttt	tagtccttgc	cctgccgaag	atattattcc	gggacgtcgt	480
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cagctgcctt	ctgaattaag	ccttgtagca	ggggatgtgg	agaagccatc	tagcagcagg	780
cgagaggagc	ctgcagggga	ggagaggcgg	cgcccagaca	ctttgcagtt	gtggcaggaa	840
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<210> 361

<211> 495

<212> DNA

<213> Mouse

<400> 361

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ggacagaggc	ccctctgttc	cccagggcct	gctgaaggca	gcgagaagca	gcggccaact	120
caacttggcg	ggaaggaacc	tcgggggaagt	ccctcagtgt	gtttggagaa	taaatgtgga	180
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ccgactcttg	cctgccctta	ctgttcttga	tatacatgat	aatcagctga	catctcttcc	360
ttcagctata	agagagctag	acaatcttca	gaaacttaat	gtcagccata	acaaactgaa	420
aatactgcct	gaagaaatta	caagcttaaa	aaacctgagg	acgctgcacc	tccagcacia	480
tgagctgact	tgcat					495

<210> 362

<211> 349

<212> DNA

<213> Mouse

<400> 362

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agtagtatgg	cggccttcct	tgtaacaggg	ttttcttttt	ctctcttcgt	ggtgcttggg	120
atggaaccca	gggctttgtt	taggcctgac	aaggctctgc	ccctgagctg	tgccaagccc	180
acctccctct	gtgtacaaag	ctcctttctt	gggtgaccaa	catcttcctg	tctttgagca	240
accaaggcca	gatgcgagcc	accagaagt	taattaaacc	aggttcatcg	ggagtttgct	300
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<210> 363

<211> 380

<212> DNA

<213> Mouse

<400> 363

gagtatgaag	ccagagtctt	agagaagtca	ctgagaaaag	aatccagaaa	caaagagacc	60
gacaagggtga	agctgacctg	gagggaccga	ttcccagcct	atctcaccaa	tcttgtctcc	120
atcatcttca	tgatcgagct	gacatttgca	atcgctctcg	gagttatcat	ctatagaatc	180
tccacagctg	cagccttggc	catgaactcc	tccccgtctg	tgcggtccaa	catccgggtt	240
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tacggctgca	ttgccagggtg	gctcaccaag	attgggtgagt	gccatgtgca	ggacagcata	360
ggcagcatgg	gcctagggca					380

<210> 364

<211> 351

<212> DNA

<213> Mouse

<400> 364

gcggcagaga	acgagatgcc	ggtggctgtg	ggtccctacg	ggcagtccca	gcccagctgc	60
ttcgaccgcg	tgaagatggg	ctttgtcatg	ggttgccgcc	tgggtatggc	ggccggggcc	120
ctgttcggca	ccttctcctg	tctcaggatc	ggaatgcggg	gtcgggagct	gatgggcggc	180

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ggcatacgat	gctaattagg	gcacggatgc	cctgctacac	ccaaacttcc	tcatccattt	300
cgaaccttgt	acaataaagt	ttttttcttc	ttgttaaaaa	aaaaaaaaaa	a	351

<210> 365

<211> 854

<212> DNA

<213> Rat

<400> 365

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cagccagtat	gcagccgccc	tggggcctgg	cgctccctct	gctgctcccc	tgggtggcag	120
gtggagtagg	gaccagccca	cgggattatt	ggttgccagc	actggcacac	cagcctgggg	180
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taaatgagtg	cactctgaat	acccgtagct	gcagccccc	tgccaattgc	ctcaataccc	780
aaggatcctt	caagtgcaaa	tgcaagcagg	gatacagggg	gaatggactg	cagtgttctg	840
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<210> 366

<211> 257

<212> DNA

<213> Rat

<400> 366

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agacagaacc	ggtttggttt	taatggcact	ctgaaggatt	cccacagcta	ccagaacgcc	120
cggttcgggt	catgcattgc	ctccgttcaa	gacctcaacc	aagattccta	caatgacgtg	180
gtgggtgggg	cccctcagga	ggacagccac	agaggggcca	tctacatctt	ccatggcttc	240
caaaccaaca	tcttgaa					257

<210> 367

<211> 475

<212> DNA

<213> Rat

<400> 367

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tgtggaccta	gcagtgggag	ccctgggcaa	cgctgtgggt	ttgtgggcgc	gtcccgtagt	180
tcagatcaac	gccagcctcc	actttgagcc	ttccaagatc	aacatcttcc	acaaggactg	240
caagcgcaat	ggcagggatg	ccacctgcct	ggctgccttc	ctctgcttcg	gacctatctt	300
cctggcaccc	cacttccaca	cagcaaccgt	cggcatcagg	tacaatgcaa	ccatggatga	360
gagacgggat	atgccacggg	cacatctgga	tgaggggtgca	gaccagttca	ccaacagggc	420
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<210> 368

<211> 392

<212> DNA

<213> Mouse

<400> 368

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<210> 369

<211> 824

<212> DNA

<213> Rat

<400> 369

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<210> 370

<211> 1663

<212> DNA

<213> Mouse

<400> 370

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 <212> DNA
 <213> Human

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 <212> DNA
 <213> Rat

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<211> 83
 <212> PRT
 <213> Mouse

<400> 373

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Met Pro Leu Pro Leu Leu Ala Ala Leu Cys Leu Ala Ala Ser Pro
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Ala Pro Ala Arg Ala Cys Gln Leu Pro Ser Glu Trp Arg Pro Leu Ser
          20          25          30
Glu Gly Cys Arg Ala Glu Leu Ala Glu Thr Ile Val Tyr Ala Lys Val
          35          40          45
Leu Ala Leu His Pro Glu Val Pro Gly Leu Tyr Asn Tyr Leu Pro Trp
          50          55          60
Gln Tyr Gln Ala Gly Glu Gly Gly Leu Phe Tyr Ser Ala Glu Val Glu
65          70          75          80
Met Leu Val
  
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<210> 374
 <211> 405
 <212> PRT
 <213> Mouse

<400> 374

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          20          25          30
Thr Met Gly Lys Ile Ala Val Ala Ser Lys Leu Met Trp Cys Ser Ala
          35          40          45
Ala Val Asp Ile Leu Phe Leu Leu Asp Gly Ser His Ser Ile Gly Lys
          50          55          60
Gly Ser Phe Glu Arg Ser Lys Arg Phe Ala Ile Ala Ala Cys Asp Ala
65          70          75          80
Leu Asp Ile Ser Pro Gly Arg Val Arg Val Gly Ala Leu Gln Phe Gly
          85          90          95
Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Arg Gln
          100          105          110
Glu Val Lys Glu Ser Ile Lys Gly Ile Val Phe Lys Gly Gly Arg Thr
          115          120          125
Glu Thr Gly Leu Ala Leu Lys Arg Leu Ser Arg Gly Phe Pro Gly Gly
          130          135          140
Arg Asn Gly Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly Lys
145          150          155          160
Ser Gln Gly Pro Val Ala Leu Pro Ala Lys Gln Leu Arg Glu Arg Gly
          165          170          175
Ile Val Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Asp Glu Leu
          180          185          190
Leu Thr Leu Ala Ser Glu Pro Lys Asp Arg His Val Leu Leu Ala Glu
          195          200          205
Gln Val Glu Asp Ala Thr Asn Gly Leu Leu Ser Thr Leu Ser Ser Ser
          210          215          220
Ala Leu Cys Thr Thr Ala Asp Pro Asp Cys Arg Val Glu Pro His Pro
225          230          235          240
Cys Glu Arg Arg Thr Leu Glu Thr Val Arg Glu Leu Ala Gly Asn Ala
          245          250          255
Leu Cys Trp Arg Gly Ser Arg Gln Ala Asp Thr Val Leu Ala Leu Pro
          260          265          270
Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Gln Thr His Pro Ala Asn
          275          280          285
Cys Tyr Arg Thr Ile Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys Gln
  
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290 295 300
 Asn Gly Gly Thr Cys Ile Pro Glu Gly Val Asp Arg Tyr His Cys Leu
 305 310 315 320
 Cys Pro Leu Ala Phe Gly Gly Glu Val Asn Cys Ala Pro Lys Leu Ser
 325 330 335
 Leu Glu Cys Arg Ile Asp Val Leu Phe Leu Leu Asp Ser Ser Ala Gly
 340 345 350
 Thr Thr Leu Gly Gly Phe Arg Arg Ala Lys Ala Phe Val Lys Arg Phe
 355 360 365
 Val Gln Ala Val Leu Arg Glu Asp Ser Arg Ala Arg Val Gly Ile Ala
 370 375 380
 Ser Tyr Gly Arg Asn Leu Met Val Ala Val Pro Cys Arg Gly Val Pro
 385 390 395 400
 Ala Leu Cys Arg Thr
 405

<210> 375
 <211> 180
 <212> PRT
 <213> Mouse

<400> 375
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 Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Asn Asn Gln Leu Leu Gly
 35 40 45
 Thr Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
 50 55 60
 Asp Gln Leu Val Asn Gln Gly Thr Pro Glu Pro Thr Glu His Pro His
 65 70 75 80
 Pro Ser Gly Gly Asn Asp Asp Lys Ala Glu Glu Thr Ser Asp Ser Gly
 85 90 95
 Gly Asp Ala Thr Gly Glu Pro Gly Ala Arg Gly Glu Met Glu Pro Ser
 100 105 110
 Leu Glu His Leu Leu Asp Ile Gln Gly Leu Pro Lys Arg Gln Ala Gly
 115 120 125
 Leu Gly Ser Ser Arg Pro Glu Ala Pro Leu Gly Leu Asp Asp Gly Ser
 130 135 140
 Cys Leu Ser Pro Ser Pro Ser Leu Ile Asn Val Arg Leu Lys Phe Leu
 145 150 155 160
 Asn Asp Thr Glu Glu Leu Ala Val Ala Arg Pro Glu Asp Thr Val Gly
 165 170 175
 Thr Leu Lys Arg
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<210> 376
 <211> 68
 <212> PRT
 <213> Mouse

<400> 376
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 His Leu Pro Leu Ile Pro Ser Val Gly Lys Ser Gln Cys Thr Gln Met
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 Trp His Cys Cys Met Pro Trp Val Cys Val Gly Asp Cys Leu Cys Leu
 35 40 45
 Ser Asp Pro Leu Trp Leu Cys Leu Leu Lys Glu Thr Glu Thr Pro Cys
 50 55 60

Gly Phe Leu Ser
65

<210> 377
<211> 107
<212> PRT
<213> Rat

<400> 377
Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Val Cys Val Leu Leu
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Pro Leu His His Gly Ala Pro Gly Pro Glu Gly Thr Ala Pro Asp Pro
20 25 30
Ala His Tyr Arg Glu Arg Val Lys Ala Met Phe Tyr His Ala Tyr Asp
35 40 45
Ser Tyr Leu Glu Asn Ala Phe Pro Tyr Asp Glu Leu Arg Pro Leu Thr
50 55 60
Cys Asp Gly His Asp Thr Trp Gly Ser Phe Ser Leu Thr Leu Ile Asp
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Ala Leu Asp Thr Leu Leu Ile Leu Gly Asn Thr Ser Glu Phe Gln Arg
85 90 95
Val Val Glu Val Leu Gln Asp Lys Arg Gly Leu
100 105

<210> 378
<211> 95
<212> PRT
<213> Rat

<400> 378
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20 25 30
Glu Gly Leu Cys Arg Leu Trp Thr Ala Thr Cys His Ser Arg Gly Glu
35 40 45
Ser Glu Val Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln
50 55 60
Gly Ser Leu Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys
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<210> 379
<211> 138
<212> PRT
<213> Mouse

<400> 379
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Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
35 40 45
Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
50 55 60
Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65 70 75 80
Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
85 90 95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
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 Arg Ser Ser Leu Asp Asp Leu Ser Ile Val Gly Gln Val Lys Arg Ile
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 His Gln Phe Val Glu Cys Leu Lys Leu Asn
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<210> 380

<211> 81

<212> PRT

<213> Rat

<400> 380

Met Ala Ser Ser Ser Asn Trp Leu Ser Gly Val Asn Val Val Leu Val
 1 5 10 15
 Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe Ile Phe Val Lys
 20 25 30
 Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg Gly Pro His Val
 35 40 45
 Pro Val Gly His Asn Ala Pro Lys Asp Leu Lys Glu Glu Ile Asp Ile
 50 55 60
 Arg Leu Ser Arg Val Gln Asp Ile Lys Tyr Glu Pro Gln Leu Leu Ala
 65 70 75 80
 Asp

<210> 381

<211> 257

<212> PRT

<213> Mouse

<400> 381

Met Arg Ser Gly Ala Leu Trp Pro Leu Leu Trp Gly Ala Leu Val Trp
 1 5 10 15
 Thr Val Gly Ser Val Gly Ala Val Met Gly Ser Glu Asp Ser Val Pro
 20 25 30
 Gly Gly Val Cys Trp Leu Gln Gln Gly Arg Glu Ala Thr Cys Ser Leu
 35 40 45
 Val Leu Lys Thr Arg Val Ser Arg Glu Glu Cys Cys Ala Ser Gly Asn
 50 55 60
 Ile Asn Thr Ala Trp Ser Asn Phe Thr His Pro Gly Asn Lys Ile Ser
 65 70 75 80
 Leu Leu Gly Phe Leu Gly Leu Val His Cys Leu Pro Cys Lys Asp Ser
 85 90 95
 Cys Asp Gly Val Glu Cys Gly Pro Gly Lys Ala Cys Arg Met Leu Gly
 100 105 110
 Gly Arg Pro Thr Leu Arg Ser Cys Val Pro Asn Cys Glu Gly Leu Pro
 115 120 125
 Ala Gly Phe Gln Val Cys Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu
 130 135 140
 Cys Glu Leu Arg Thr Ala Arg Cys Arg Gly His Pro Asp Leu Arg Val
 145 150 155 160
 Met Tyr Arg Gly Arg Cys Gln Lys Ser Cys Ala Gln Val Val Cys Pro
 165 170 175
 Arg Pro Gln Ser Cys Leu Val Asp Gln Thr Gly Ser Ala His Cys Val
 180 185 190
 Val Cys Arg Ala Ala Pro Cys Pro Val Pro Ser Asn Pro Gly Gln Glu
 195 200 205
 Leu Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Leu Arg
 210 215 220
 Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Pro Gly

225 230 235 240
 Ile Cys Thr Gly Gly Pro Lys Val Pro Ala Glu Glu Glu Glu Asn Phe
 245 250 255
 Val

<210> 382
 <211> 285
 <212> PRT
 <213> Rat

<400> 382
 Met Ile Ser Trp Met Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
 1 5 10 15
 Pro Met Leu Gly Ala Phe Ala Arg Arg Asp Phe Gln Lys Gly Gly Pro
 20 25 30
 Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
 35 40 45
 Gly Ala Pro Gly Ser Ser Gly Met Val Gly Arg Met Gly Phe Pro Gly
 50 55 60
 Lys Asp Gly Gln Asp Gly Gln Asp Gly Asp Arg Gly Asp Ser Gly Glu
 65 70 75 80
 Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Gln Gly Pro Lys
 85 90 95
 Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly
 100 105 110
 Val Ser Gly Thr Pro Gly Lys His Gly Ile Pro Gly Lys Lys Gly Pro
 115 120 125
 Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly
 130 135 140
 Ser Ser Arg Ala Lys Ser Ala Phe Ser Val Ser Val Thr Lys Ser Tyr
 145 150 155 160
 Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu
 165 170 175
 Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Ser Val Pro
 180 185 190
 Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu
 195 200 205
 Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp
 210 215 220
 Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala
 225 230 235 240
 Leu Lys Glu Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln
 245 250 255
 Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly
 260 265 270
 Phe Leu Ile Tyr Ala Asp Gln Gly Asp Pro Asn Glu Val
 275 280 285

<210> 383
 <211> 183
 <212> PRT
 <213> Rat

<400> 383
 Met Lys Leu Leu Cys Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1 5 10 15
 Pro Ala Gln Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 130 135 140
 Ile Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175
 Asp Arg His Lys Met Leu Ser
 180

<210> 384
 <211> 292
 <212> PRT
 <213> Mouse

<400> 384
 Cys Gln Leu Pro Leu Arg Val Leu Ile Ile Ser Asn Asn Lys Leu Gly
 1 5 10 15
 Ala Leu Pro Pro Asp Ile Ser Thr Leu Gly Ser Leu Arg Gln Leu Asp
 20 25 30
 Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Val Glu Leu Cys Ser Leu
 35 40 45
 Arg Ser Leu Arg Asp Leu Asn Val Arg Arg Asn Gln Leu Ser Thr Leu
 50 55 60
 Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Arg Leu Asp Phe Ser Cys
 65 70 75 80
 Asn Arg Ile Ser Arg Ile Pro Val Ser Phe Cys Arg Leu Arg His Leu
 85 90 95
 Gln Val Val Leu Leu Asp Ser Asn Pro Leu Gln Ser Pro Pro Ala Gln
 100 105 110
 Ile Cys Leu Lys Gly Lys Leu His Ile Phe Lys Tyr Leu Thr Met Glu
 115 120 125
 Ala Gly Arg Arg Gly Ala Ala Leu Gly Asp Leu Val Pro Ser Arg Pro
 130 135 140
 Pro Ser Phe Ser Pro Cys Pro Ala Glu Asp Leu Phe Pro Gly Arg Arg
 145 150 155 160
 Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser Gly Ser
 165 170 175
 Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu Leu Ser
 180 185 190
 Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg Gln Pro
 195 200 205
 Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp Phe Ile
 210 215 220
 Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala Glu Glu
 225 230 235 240
 Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu Lys Pro
 245 250 255
 Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg Arg Pro
 260 265 270
 Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln Gln
 275 280 285

Ser Gly Gly Trp
290

<210> 385
<211> 164
<212> PRT
<213> Mouse

<400> 385
Ser Arg Gln Leu Arg Ala Pro Arg Phe Asp Pro Arg Ala Gly Phe His
1 5 10 15
Ala Glu Gly Lys Asp Arg Gly Pro Ser Val Pro Gln Gly Leu Leu Lys
20 25 30
Ala Ala Arg Ser Ser Gly Gln Leu Asn Leu Ala Gly Arg Asn Leu Gly
35 40 45
Glu Val Pro Gln Cys Val Trp Arg Ile Asn Val Asp Ile Pro Glu Glu
50 55 60
Ala Asn Gln Asn Leu Ser Phe Ser Ser Thr Glu Arg Trp Trp Asp Gln
65 70 75 80
Thr Asp Leu Thr Lys Leu Ile Ile Ser Ser Asn Lys Leu Gln Ser Leu
85 90 95
Ser Asp Asp Leu Arg Leu Leu Pro Ala Leu Thr Val Leu Asp Ile His
100 105 110
Asp Asn Gln Leu Thr Ser Leu Pro Ser Ala Ile Arg Glu Leu Asp Asn
115 120 125
Leu Gln Lys Leu Asn Val Ser His Asn Lys Leu Lys Ile Leu Pro Glu
130 135 140
Glu Ile Thr Ser Leu Lys Asn Leu Arg Thr Leu His Leu Gln His Asn
145 150 155 160
Glu Leu Thr Cys

<210> 386
<211> 71
<212> PRT
<213> Mouse

<400> 386
Ser Leu Ser Ile Leu Pro Ala Val Arg Val Ser Pro Arg Pro Thr Tyr
1 5 10 15
Pro Ser Thr Ala Ser Ser Met Ala Ala Phe Leu Val Thr Gly Phe Phe
20 25 30
Phe Ser Leu Phe Val Val Leu Gly Met Glu Pro Arg Ala Leu Phe Arg
35 40 45
Pro Asp Lys Ala Leu Pro Leu Ser Cys Ala Lys Pro Thr Ser Leu Cys
50 55 60
Val Gln Ser Ser Phe Leu Gly
65 70

<210> 387
<211> 126
<212> PRT
<213> Mouse

<400> 387
Glu Tyr Glu Ala Arg Val Leu Glu Lys Ser Leu Arg Lys Glu Ser Arg
1 5 10 15
Asn Lys Glu Thr Asp Lys Val Lys Leu Thr Trp Arg Asp Arg Phe Pro
20 25 30
Ala Tyr Phe Thr Asn Leu Val Ser Ile Ile Phe Met Ile Ala Val Thr
35 40 45

Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg Ile Ser Thr Ala Ala
 50 55 60
 Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg Ser Asn Ile Arg Val
 65 70 75 80
 Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu Val Val Ile Ile Leu
 85 90 95
 Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp Leu Thr Lys Ile Gly
 100 105 110
 Glu Cys His Val Gln Asp Ser Ile Gly Ser Met Gly Leu Gly
 115 120 125

<210> 388

<211> 84

<212> PRT

<213> Rat

<400> 388

Ala Ala Glu Asn Glu Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser
 1 5 10 15
 Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly Phe Val Met Gly Cys
 20 25 30
 Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu
 35 40 45
 Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr
 50 55 60
 Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met
 65 70 75 80
 Gly Ile Arg Cys

<210> 389

<211> 284

<212> PRT

<213> Rat

<400> 389

Gly Gly Ser Ser Val Ser His Val Leu Arg Gly Ser Gly Gln Glu Arg
 1 5 10 15
 Ser Pro Pro Pro Ala Ser Met Gln Pro Pro Trp Gly Leu Ala Leu Pro
 20 25 30
 Leu Leu Leu Pro Trp Val Ala Gly Gly Val Gly Thr Ser Pro Arg Asp
 35 40 45
 Tyr Trp Leu Pro Ala Leu Ala His Gln Pro Gly Val Cys His Tyr Gly
 50 55 60
 Thr Lys Thr Ala Cys Cys Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val
 65 70 75 80
 Cys Glu Ala Val Cys Glu Pro Arg Cys Lys Phe Gly Glu Cys Val Gly
 85 90 95
 Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser
 100 105 110
 Gln Asp Val Asn Glu Cys Ala Phe Lys Pro Arg Pro Cys Gln His Arg
 115 120 125
 Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His
 130 135 140
 Met Leu Leu Pro Asp Ala Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg
 145 150 155 160
 Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys
 165 170 175
 Val Cys Pro Ser Ser Gly Leu Arg Leu Gly Pro Asn Gly Arg Val Cys
 180 185 190
 Leu Asp Ile Asp Glu Cys Ala Ser Ser Lys Ala Val Cys Pro Ser Asn

195	200	205
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile		
210	215	220
Gly Phe Glu Leu Lys Tyr Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile		
225	230	235
Asn Glu Cys Thr Leu Asn Thr Arg Thr Cys Ser Pro His Ala Asn Cys		240
	245	250
Leu Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg		255
	260	265
Gly Asn Gly Leu Gln Cys Ser Val Ile Pro Glu His		270
275	280	

<210> 390
 <211> 85
 <212> PRT
 <213> Rat

<400> 390
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
1 5 10 15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
20 25 30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
35 40 45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
50 55 60
Pro Gln Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65 70 75 80
Gln Thr Asn Ile Leu
85

<210> 391
 <211> 158
 <212> PRT
 <213> Rat

<400> 391
Phe Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser
1 5 10 15
Glu Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln
20 25 30
Leu Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu
35 40 45
Gly Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala
50 55 60
Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
65 70 75 80
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
85 90 95
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
100 105 110
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
115 120 125
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
130 135 140
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu
145 150 155

<210> 392
 <211> 124
 <212> PRT

<213> Mouse

<400> 392

Ala Ala Glu Gln Glu Ala Ser Ser Arg Arg Arg Arg Gly Gly Ala Gly
 1 5 10 15
 Pro Ala Leu Phe Ser Ser Gly Ser Leu Arg Ser Glu Pro Gln Pro Arg
 20 25 30
 Leu Pro Gln Ala Arg Ser Arg Pro Arg Pro Ser Phe Leu Gln Ala Arg
 35 40 45
 Ser Arg Pro Cys Leu Ser Gln Ala Cys Ser Pro Ala Ala Ser Val Leu
 50 55 60
 Ser Ser Ser Ser Leu Cys Gly Arg Ser His Leu Leu Pro Gly Ser Leu
 65 70 75 80
 Pro Ala Thr Ala Phe Leu Leu Leu Leu Pro Gly Ser Leu Pro Gly Arg
 85 90 95
 Arg Pro Ser Ala Gln Ala Ala Pro Val Leu Ala Trp Gly Leu Val
 100 105 110
 Ala Phe Gln Leu Gly Val Ala Ala Gly Ala Gly Arg
 115 120

<210> 393

<211> 242

<212> PRT

<213> Rat

<400> 393

Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
 1 5 10 15
 Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
 20 25 30
 Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
 35 40 45
 Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys
 50 55 60
 Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
 65 70 75 80
 Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
 85 90 95
 Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Pro Cys Lys
 100 105 110
 Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
 115 120 125
 Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
 130 135 140
 Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
 145 150 155 160
 Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
 165 170 175
 Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
 180 185 190
 Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
 195 200 205
 Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
 210 215 220
 Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
 225 230 235 240
 Gly Arg

<210> 394

<211> 99

<212> PRT

<213> Mouse

<400> 394

```

Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Cys
 1          5          10          15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
          20          25          30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
          35          40          45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
          50          55          60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
65          70          75          80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
          85          90          95
Tyr Glu Glu

```

<210> 395

<211> 103

<212> PRT

<213> Human

<400> 395

```

Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
 1          5          10          15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
          20          25          30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
          35          40          45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
          50          55          60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
65          70          75          80
Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
          85          90          95
Ser Gly Glu Arg Arg Pro Leu
          100

```

<210> 396

<211> 1529

<212> PRT

<213> Rat

<400> 396

```

Met Ser Gly Ile Gly Trp Gln Thr Leu Ser Leu Ser Leu Ala Leu Val
 1          5          10          15
Leu Ser Ile Leu Asn Lys Val Ala Pro His Ala Cys Pro Ala Gln Cys
          20          25          30
Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
          35          40          45
Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
          50          55          60
Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
65          70          75          80
Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
          85          90          95
Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
          100          105          110
Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys

```

161

Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn	Arg	Ile	Ser	Cys	Val	Gly	Asn	Asp
610						615					620				
Ser	Phe	Thr	Gly	Leu	Gly	Ser	Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn
625					630					635					640
Gln	Ile	Thr	Thr	Val	Ala	Pro	Gly	Ala	Phe	Gly	Thr	Leu	His	Ser	Leu
				645					650					655	
Ser	Thr	Leu	Asn	Leu	Leu	Ala	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu
			660					665					670		
Ala	Trp	Leu	Gly	Glu	Trp	Leu	Arg	Arg	Lys	Arg	Ile	Val	Thr	Gly	Asn
			675				680					685			
Pro	Arg	Cys	Gln	Lys	Pro	Tyr	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp
						695					700				
Val	Ala	Ile	Gln	Asp	Phe	Thr	Cys	Asp	Asp	Gly	Asn	Asp	Asp	Asn	Ser
705					710					715					720
Cys	Ser	Pro	Leu	Ser	Arg	Cys	Pro	Ser	Glu	Cys	Thr	Cys	Leu	Asp	Thr
				725					730					735	
Val	Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Lys	Val	Leu	Pro	Lys	Gly	Ile
			740					745					750		
Pro	Arg	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Asp	Gly	Asn	Gln	Phe	Thr	Leu
			755				760					765			
Val	Pro	Lys	Glu	Leu	Ser	Asn	Tyr	Lys	His	Leu	Thr	Leu	Ile	Asp	Leu
			770			775					780				
Ser	Asn	Asn	Arg	Ile	Ser	Thr	Leu	Ser	Asn	Gln	Ser	Phe	Ser	Asn	Met
785					790					795					800
Thr	Gln	Leu	Leu	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	Leu	Arg	Cys	Ile
				805					810					815	
Pro	Pro	Arg	Thr	Phe	Asp	Gly	Leu	Lys	Ser	Leu	Arg	Leu	Leu	Ser	Leu
			820					825					830		
His	Gly	Asn	Asp	Ile	Ser	Val	Val	Pro	Glu	Gly	Ala	Phe	Gly	Asp	Leu
		835					840					845			
Ser	Ala	Leu	Ser	His	Leu	Ala	Ile	Gly	Ala	Asn	Pro	Leu	Tyr	Cys	Asp
		850				855				860					
Cys	Asn	Met	Gln	Trp	Leu	Ser	Asp	Trp	Val	Lys	Ser	Glu	Tyr	Lys	Glu
865					870					875					880
Pro	Gly	Ile	Ala	Arg	Cys	Ala	Gly	Pro	Gly	Glu	Met	Ala	Asp	Lys	Leu
				885					890					895	
Leu	Leu	Thr	Thr	Pro	Ser	Lys	Lys	Phe	Thr	Cys	Gln	Gly	Pro	Val	Asp
			900					905					910		
Val	Thr	Ile	Gln	Ala	Lys	Cys	Asn	Pro	Cys	Leu	Ser	Asn	Pro	Cys	Lys
		915					920					925			
Asn	Asp	Gly	Thr	Cys	Asn	Asn	Asp	Pro	Val	Asp	Phe	Tyr	Arg	Cys	Thr
		930				935					940				
Cys	Pro	Tyr	Gly	Phe	Lys	Gly	Gln	Asp	Cys	Asp	Val	Pro	Ile	His	Ala
945					950					955					960
Cys	Ile	Ser	Asn	Pro	Cys	Lys	His	Gly	Gly	Thr	Cys	His	Leu	Lys	Glu
			965						970					975	
Gly	Glu	Asn	Asp	Gly	Phe	Trp	Cys	Thr	Cys	Ala	Asp	Gly	Phe	Glu	Gly
			980				985					990			
Glu	Ser	Cys	Asp	Ile	Asn	Ile	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	Glu
			995				1000					1005			
Asn	Asn	Ser	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Thr	Cys	Leu	Cys
			1010			1015					1020				
Pro	Pro	Glu	Tyr	Thr	Gly	Glu	Leu	Cys	Glu	Glu	Lys	Leu	Asp	Phe	Cys
1025					1030					1035					104
Ala	Gln	Asp	Leu	Asn	Pro	Cys	Gln	His	Asp	Ser	Lys	Cys	Ile	Leu	Thr
				1045					1050					1055	
Pro	Lys	Gly	Phe	Lys	Cys	Asp	Cys	Thr	Pro	Gly	Tyr	Ile	Gly	Glu	His
			1060					1065					1070		
Cys	Asp	Ile	Asp	Phe	Asp	Asp	Cys	Gln	Asp	Asn	Lys	Cys	Lys	Asn	Gly
		1075					1080					1085			
Ala	His	Cys	Thr	Asp	Ala	Val	Asn	Gly	Tyr	Thr	Cys	Val	Cys	Pro	Glu

1090	1095	1100
Gly Tyr Ser Gly Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Leu		
1105	1110	1115
Arg Thr Ser Pro Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys		
	1125	1130
Ile Ile Arg Val Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu		
	1140	1145
Gly Glu Lys Cys Glu Lys Leu Val Ser Val Asn Phe Val Asn Lys Glu		
	1155	1160
Ser Tyr Leu Gln Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile		
	1170	1175
Thr Leu Gln Ile Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys		
1185	1190	1195
Gly Asp Lys Asp His Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg		
	1205	1210
Ala Ser Tyr Asp Thr Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val		
	1220	1225
Glu Thr Ile Asn Asp Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu		
	1235	1240
Asp Ser Ser Leu Ser Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile		
	1250	1255
Thr Asn Leu Ser Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr		
1265	1270	1275
Val Gly Gly Met Pro Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala		
	1285	1290
Pro Gly Gln Asn Gly Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr		
	1300	1305
Ile Asn Ser Glu Leu Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly		
	1315	1320
Ile Leu Pro Gly Cys Glu Pro Cys His Lys Lys Val Cys Ala His Gly		
	1330	1335
Thr Cys Gln Pro Ser Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu		
1345	1350	1355
Gly Trp Met Gly Pro Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu		
	1365	1370
Gly Asn Lys Cys Val His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser		
	1380	1385
Tyr Ser Cys Lys Cys Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu		
	1395	1400
Glu Glu Asp Leu Phe Asn Pro Cys Gln Val Ile Lys Cys Lys His Gly		
	1410	1415
Lys Cys Arg Leu Ser Gly Leu Gly Gln Pro Tyr Cys Glu Cys Ser Ser		
1425	1430	1435
Gly Phe Thr Gly Asp Ser Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu		
	1445	1450
Arg Ile Arg Asp Tyr Tyr Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln		
	1460	1465
Thr Thr Lys Lys Val Ser Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly		
	1475	1480
Gly Gln Cys Cys Gly Pro Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe		
	1490	1495
Glu Cys Thr Asp Gly Ser Ser Phe Val Asp Glu Val Glu Lys Val Val		
1505	1510	1515
Lys Cys Gly Cys Thr Arg Cys Ala Ser		
	1525	

<210> 397

<211> 8

<212> PRT

<213> Mouse

<400> 397

Trp Tyr Asn Ala Trp Asn Glu Lys
1 5

<210> 398

<211> 7

<212> PRT

<213> Mouse

<400> 398

Met Val Ile Ile Thr Thr Lys
1 5

<210> 399

<211> 2206

<212> DNA

<213> Rat

<400> 399

gtttcgtctt	aacgccctct	ctgcgttggc	agaactggcc	gtgggctccc	gctggtacca	60
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atccgcggtg	actgcaagta	ccggtctcct	gtggaagaag	gctcacgcag	aatctccacc	180
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 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
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 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
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 Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp
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 Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys
 385 390 395 400
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ 99/00051

A. CLASSIFICATION OF SUBJECT MATTER												
Int Cl ⁶ : C12N 15/12, 15/18, 15/19												
According to International Patent Classification (IPC) or to both national classification and IPC												
B. FIELDS SEARCHED												
Minimum documentation searched (classification system followed by classification symbols) C12N 15/12, 15/18, 15/19												
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched												
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) GenBank, GenBank (ESTs), EMBL, EMBL (ESTs), SwissProt, TREMBL, PIR.												
C. DOCUMENTS CONSIDERED TO BE RELEVANT												
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.										
X	GenBank (ESTs) Accession no AI412233	SEQ ID NO 119 Claims 1-17, 19, 21, 23, 25, 27, 28										
X	GenBank (ESTs) Accession noAA850731	SEQ ID NO 119 Claims 1-17, 19, 21, 23, 25, 27, 28										
X	GenBank (ESTs) Accession no AI299847	SEQ ID NO 119 Claims 1-17, 19, 21, 23, 25, 27, 28										
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input type="checkbox"/> See patent family annex												
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td>"A" document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E" earlier application or patent but published on or after the international filing date</td> <td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O" document referring to an oral disclosure, use, exhibition or other means</td> <td>"&" document member of the same patent family</td> </tr> <tr> <td>"P" document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	"P" document published prior to the international filing date but later than the priority date claimed	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention											
"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone											
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art											
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family											
"P" document published prior to the international filing date but later than the priority date claimed												
Date of the actual completion of the international search 8 September 1999		Date of mailing of the international search report 15 SEP 1999										
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer GILLIAN ALLEN Telephone No.: (02) 6283 2266										

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ 99/00051

Box 1 Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-28
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
It is not economically feasible to carry out a full search on all sequences of the claims. Search has been limited to sequences from each of the Examples, namely: -
SEQ ID NOs 68, 118 and 196 from Example 3; SEQ ID NOs 119 and 197 from Example 5; SEQ ID NOs 263, 270 and 344 from Example 5; SEQ ID NOs 273 and 347 from Example 6; SEQ ID NO 129 from Example 7
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ 99/00051

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank (ESTs) Accession no W97325	SEQ ID NO 263 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AA111146	SEQ ID NO 263 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AI037414	SEQ ID NO 263 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AI282114	SEQ ID NO 270 Claim nos Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AA865643	SEQ ID NO 270 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AI140104	SEQ ID NO 270 Claim nos 1-9, 11, 13, 16, 17, 19, 21, 22-28
X	GenBank (ESTs) Accession no AA726580	SEQ ID NO 273 Claim nos 1-9, 11, 17, 19, 21, 23, 25, 27
X	GenBank (ESTs) Accession no AA407924	SEQ ID NO 273 Claim nos 1-9, 11, 17, 19, 21, 23, 25, 27
X	GenBank (ESTs) Accession no AA498629	SEQ ID NO 273 Claim nos 1-9, 11, 17, 19, 21, 23, 25, 27

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